

SEARCH REQUEST FORM

78/92

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

Date completed: 10/21/92
Searcher: Jan
Terminal time: _____
Elapsed time: 10
CPU time: +10
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

____ STIC
____ ☒ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ ☒ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ ☒ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 27 Seconds
(without alignments)
1275.037 Million cell updates/sec

Title: US-09-823-307c-2

Perfect score: 1082
Sequence: 1 MKSGLMYFFLCIRIKVLTG.....YFMRAVNTAKSRITDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organeller:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeal:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	4	O9Y6W8 homo sapien
2	737.5	68.2	200	11	O9Y6W8 mus musculu
3	734	67.8	200	11	O9Y6W8 mus musculu
4	701	64.8	200	11	O9Y6W8 mus musculu
5	696	64.3	216	11	O9Y6W8 mus musculu
6	146.5	13.5	221	11	O9Y6W8 mus musculu
7	145.5	13.4	221	11	O9Y6W8 mus musculu
8	145.5	13.4	221	11	O9Y6W8 mus musculu
9	145	13.4	219	6	O9Y6W8 mus musculu
10	140.5	13.0	221	6	O9Y6W8 mus musculu
11	140.5	13.0	221	6	O9Y6W8 mus musculu
12	139.5	12.9	173	6	O9Y6W8 mus musculu
13	136.5	12.6	220	6	O9Y6W8 mus musculu
14	135.5	12.5	220	6	O9Y6W8 mus musculu
15	130.5	12.1	220	6	O9Y6W8 mus musculu
16	125.5	11.6	220	6	O9Y6W8 mus musculu

17	115.5	10.7	220	6	O9Y6W8 mus musculu
18	103.5	9.6	988	5	O9Y6W8 mus musculu
19	91.5	8.5	485	5	O9Y6W8 mus musculu
20	87	8.0	223	6	O9Y6W8 mus musculu
21	84.5	7.8	209	4	O9Y6W8 mus musculu
22	84.5	7.8	223	11	O9Y6W8 mus musculu
23	84	7.8	223	4	O9Y6W8 mus musculu
24	84	7.8	285	17	O9Y6W8 mus musculu
25	84	7.8	419	13	O9Y6W8 mus musculu
26	83.5	7.7	223	11	O9Y6W8 mus musculu
27	83	7.7	1239	10	O9Y6W8 mus musculu
28	82.5	7.6	223	6	O9Y6W8 mus musculu
29	82	7.6	223	6	O9Y6W8 mus musculu
30	82	7.6	223	6	O9Y6W8 mus musculu
31	81	7.5	276	12	O9Y6W8 mus musculu
32	81	7.5	276	12	O9Y6W8 mus musculu
33	81	7.5	680	11	O9Y6W8 mus musculu
34	80.5	7.4	247	16	O9Y6W8 mus musculu
35	80.5	7.4	635	11	O9Y6W8 mus musculu
36	80.5	7.4	635	11	O9Y6W8 mus musculu
37	79.5	7.3	269	4	O9Y6W8 mus musculu
38	79	7.3	370	4	O9Y6W8 mus musculu
39	78.5	7.3	310	11	O9Y6W8 mus musculu
40	78	7.2	231	5	O9Y6W8 mus musculu
41	77.5	7.2	311	11	O9Y6W8 mus musculu
42	77.5	7.1	323	6	O9Y6W8 mus musculu
43	77	7.1	338	5	O9Y6W8 mus musculu
44	77	7.1	539	12	O9Y6W8 mus musculu
45	77	7.1	619	10	O9Y6W8 mus musculu

ALIGNMENTS

RESULT 1			
ID	Q9Y6W8	PRELIMINARY;	PRT; 199 AA.
AC	Q9Y6W8		
AD	Q9Y6W8		
AE	Q9Y6W8		
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AG	Q9Y6W8		
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MEDLINE-20243570:
RA Aicher A., Hayden-Jeddelier M., Brady W.A., Pezzullo A., Richter G.,
RA Magaletti D., Buckwalter S., Jeddelier J.A., Clark P.A.,
RT "Characterization of human inducible costimulator ligand expression
RT and function."
RU J. Immunol. 164:4699-4696(2000).
DR EMBL: AB023135; BA82129.1;
DR EMBL: AJ277632; CAC06642.1;
DR EMBL: AF218312; AAF1301.1;
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 199 AA; 22624 MM; 214EC74IC9BDC9PC CRC64;
Query Match 100.0%; Score 1082; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 2,8e-109;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K S G L W F F L F C L R I K V L T G E I N S A N Y E M F I F H N G G V O I L C K Y P D I V O O F K M O L L K G G Q 60
1 M K S G L W F F L F C L R I K V L T G E I N S A N Y E M F I F H N G G V O I L C K Y P D I V O O F K M O L L K G G Q 60
DB 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120
61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120
QY 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L C I L C W L T K R K K S S V H D P N G E Y 180
121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L C I L C W L T K R K K S S V H D P N G E Y 180
DB 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L C I L C W L T K R K K S S V H D P N G E Y 180
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181 M E M R A V N T A K K S R L T D V T L 199
DB 181 M E M R A V N T A K K S R L T D V T L 199

RESULT 2
09WVS0 PRELIMINARY: PRT: 200 AA.
AC 09WVS0:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDATORY MOLECULE ALLIN
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
GN CCLP OR ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
RT transmission."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Wu D., Gannon M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
RA Matis L.A., Rother R.P.;
RT "CCLP, A novel molecule that regulates T cell activation."
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Hughes H.W., Hulcok A., Heuck C., Buchner K., Hummelbauer H.,
RA Oliveri F., Krocsek R.A.;
RT "Molecular cloning and characterization of murine ICOS and
RT identification of B7 as ICOS ligand."
RL Eur. J. Immunol. 30:1040-1047(2000).
DR EMBL: AB023132; BA82126.1;
DR EMBL: AF257230; AAF0099.1;

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DR EMBL: AJ250559; CAB7153.1;
DR MGD: MGI:1858745; ICOS.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22690 MM; 9B2276E4CAB1DB47 CRC64;
Query Match 68.2%; Score 737.5; DB 11; Length 200;
Best Local Similarity 69.3%; Pred. No. 6e-72;
Matches 138; Conservative 20; Mismatches 40; Indels 1; Gaps 1;

QY 1 M K S G L W F F L F C L R I K V L T G E I N S A N Y E M F I F H N G G V O I L C K Y P D I V O O F K M O L L K G G Q 60
1 M K P Y C H V F F L F R L T L G E I N S A D H R M F S F H N G G V O I S C Y P E T V O O L K M L R F R E R E 60
DB 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P F K 120
61 V C E L T K T K G S G N A V S I K N P M L C L Y L S N N S V S F F L N P D S S G S Y F C S I S I F D P P P F Q 120
QY 121 V - T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L C I L C W L T K R K K S S V H D P N G E 179
121 E R N L S G Y L H I E S O L C C O L K L M L P V G C A F V V V L L F C I I L I M P S K R K K S G S V H D P N S E 180
DB 121 E R N L S G Y L H I E S O L C C O L K L M L P V G C A F V V V L L F C I I L I M P S K R K K S G S V H D P N S E 180
180 Y M F R A V N T A K K S R L T D V T 198
181 Y M F M A V N T N T K K S R L A G V T 199
DB 181 Y M F M A V N T N T K K S R L A G V T 199

RESULT 3
09JL17 PRELIMINARY: PRT: 200 AA.
AC 09JL17:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATORY PROTEIN)
DE (FRAGMENT).
GN ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL; INTRA-EPITHELIUM;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Cocchia M.A., Kohno T., Jafuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,
RA Senaldi G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS."
RT Nature 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RA McAdam A.J., Greenwald R.J., Levin M.A., Chernova T., Malenkovich N.,
RA Ling V., Freeman G.J., Sharpe A.H.;
RT "The inducible costimulatory (ICOS) molecule is critical for CD40-
RT mediated antibody class switching."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF216748; AAF45150.1;
DR EMBL: AF327185; AAG48732.1;
DR EMBL: AF327184; AAG48732.1; JOINED.
FT NON-TER
SQ SEQUENCE 200 AA; 22709 MM; 87D97F0DC44ADCA7 CRC64;
Query Match 67.8%; Score 734; DB 11; Length 200;
Best Local Similarity 70.4%; Pred. No. 1.4e-71;
Matches 138; Conservative 19; Mismatches 35; Indels 4; Gaps 2;

QY 7 Y F - - F L F C L R I K V L T G E I N S A N Y E M F I F H N G G V O I L C K Y P D I V O O F K M O L L K G G Q I L C 63
4 Y F C R V F E C F I L R L T L G E I N S A D H R M F S F H N G G V O I S C Y P E T V O O L K M L R F R E R E V L C 63

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 : Search time 14 Seconds
(without alignments)
347.192 Million cell updates/sec

Title: US-09-823-307C-2
Perfect score: 1092
Sequence: 1 MKSLMWFLECLRIKVLG.....YMFRAVNTAKRSLDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrus-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	15.1	218	3	US-08-228-208A-20
2	146.3	13.3	223	1	US-08-508-058-4
3	146.3	13.3	223	2	US-08-459-818-24
4	146.3	13.3	223	2	US-08-889-666-24
5	146.3	13.3	223	2	US-08-465-078-24
6	146.3	13.3	223	2	US-08-725-776-24
7	146.3	13.3	223	2	US-08-488-062-24
8	146.3	13.3	223	2	US-08-228-208A-19
9	134.5	12.4	220	3	US-08-228-208A-21
10	134.5	12.4	225	1	US-08-505-058-3
11	134.5	12.4	225	2	US-08-459-818-23
12	134.5	12.4	225	2	US-08-889-666-23
13	134.5	12.4	225	2	US-08-465-078-23
14	134.5	12.4	225	2	US-08-725-776-23
15	134.5	12.4	225	2	US-08-488-062-23
16	134.5	12.4	223	1	US-08-505-058-5
17	126	11.6	223	2	US-08-459-818-25
18	126	11.6	223	2	US-08-889-666-25
19	126	11.6	223	2	US-08-465-078-25
20	126	11.6	223	2	US-08-725-776-25
21	126	11.6	223	2	US-08-488-062-25
22	120.5	11.1	367	2	US-08-630-172-19
23	120.5	11.1	367	4	US-09-375-419-19
24	119.5	11.0	134	4	US-08-630-172-3
25	119.5	11.0	134	4	US-09-375-419-3
26	110.5	10.2	110	4	US-09-460-384-33
27	93	8.6	221	3	US-08-228-208A-22

28	89.5	8.3	117	2	US-08-529-878B-39	Sequence 39, Appl
29	87	8.0	330	2	US-08-332-562A-81	Sequence 81, Appl
30	87	8.0	330	2	US-08-332-562A-134	Sequence 134, Appl
31	86.5	8.0	209	4	US-09-430-503-20	Sequence 20, Appl
32	84.5	7.8	209	4	US-09-430-503-18	Sequence 18, Appl
33	84.5	7.8	209	4	US-09-430-503-24	Sequence 24, Appl
34	84	7.8	223	3	US-08-228-208A-17	Sequence 17, Appl
35	84	7.8	283	2	US-08-332-562A-136	Sequence 136, Appl
36	82.5	7.6	209	4	US-09-430-503-22	Sequence 22, Appl
37	81.5	7.5	187	1	US-08-067-684-14	Sequence 14, Appl
38	81.5	7.5	187	2	US-08-008-898-14	Sequence 14, Appl
39	81.5	7.5	187	2	US-08-459-818-14	Sequence 14, Appl
40	81.5	7.5	187	2	US-08-889-666-14	Sequence 14, Appl
41	81.5	7.5	187	2	US-08-465-078-14	Sequence 14, Appl
42	81.5	7.5	187	2	US-08-725-776-14	Sequence 14, Appl
43	81.5	7.5	187	2	US-08-488-062-14	Sequence 14, Appl
44	81.5	7.5	187	3	US-08-228-208A-14	Sequence 14, Appl
45	81.5	7.5	187	5	PCT-US95-06726-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-228-208A-20
Sequence 20, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Wallace, Phillip M.
TITLE OF INVENTION: CTLA4/CD28ig HYBRID FUSION
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA: US/08/228, 208A
APPLICATION NUMBER: 08/008, 898
CLASSIFICATION: 435
FILING DATE: 15-Apr-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/008, 898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723, 617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-300501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-228-208A-20

Query Match 15.1%; Score 163; DB 3; Length 218;
Best Local Similarity 26.5%; Pred No. 3e-11;
Matches 41; Conservative 31; Mismatches 65; Indels 18; Gaps 7;

OY 30 MEIFHNGVOILCKYPD--IVQOFKQMLKGGQILCDLTKT-KSGGNTVSIRSLK-----F 82
DB 29 LLYVDNNEVXSISCRYSYNLAKERASLYKG--VNSDVEVCVGNNGFTYQOFRPNVWG 86
OY 83 CHSOLSNNSVSFLYXNDHSHANYFCNLSIFDPPPF--KVTLTGGLHYESQLC---C 137
DB 87 CDGFPDNEVTFEFLMLNDVNHDTYFCRIEVMYPPYLDNEKSNGTIIHIKEKHLCOAQT 146
OY 138 QKFWLPIGCAAFVVC--ILGCLIC--WLTKK 168
DB 147 SPLKFWLVVAVGLCYGLTYVTLCTIWTNSR 181

RESULT 2
US-08-505-058-4
Sequence 4, Application US/08505058
Patent No. 5773253
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,058
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/228,208
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.30US11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-058-4

Query Match 13.5%; Score 146.5; DB 1; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

OY 30 MEIFHNGVOILCKYPD--IVQOFKQMLKGGQILCDLTKT-KSGGNTVSIRSLK----- 81
DB 30 LLYVDNNEVXSISCRYSYNLAKERASLYKG--VNSDVEVCVGNNGFTYQOFRPNVWG 87
OY 82 -FCHSOLSNNSVSFLYXNDHSHANYFCNLSIFDPPPF--KVTLTGGLHYESQLC--- 136
DB 82 -FCHSOLSNNSVSFLYXNDHSHANYFCNLSIFDPPPF--KVTLTGGLHYESQLC--- 136

DB 88 FNCODNFDNEVTFEFLMLNDVNHDTYFCRIEVMYPPYLDNEKSNGTIIHIKEKHLCOA 147
OY 137 ---COLKFWLPIGCAAFVVC--ILGCLIC--WLTKK 168
DB 148 XXXQTSPLKFWLVVAVGLCYGLTYVTLCTIWTNSR 187

RESULT 3
US-08-459-818-24
Sequence 24, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damsle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ. ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-24

Query Match 13.5%; Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%; Pred. No. 2.7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

OY 30 MEIFHNGVOILCKYPD--IVQOFKQMLKGGQILCDLTKT-KSGGNTVSIRSLK----- 81
DB 30 LLYVDNNEVXSISCRYSYNLAKERASLYKG--VNSDVEVCVGNNGFTYQOFRPNVWG 87
OY 82 -FCHSOLSNNSVSFLYXNDHSHANYFCNLSIFDPPPF--KVTLTGGLHYESQLC--- 136
DB 88 FNCODNFDNEVTFEFLMLNDVNHDTYFCRIEVMYPPYLDNEKSNGTIIHIKEKHLCOA 147
OY 137 ---COLKFWLPIGCAAFVVC--ILGCLIC--WLTKK 168
DB 148 XXXQTSPLKFWLVVAVGLCYGLTYVTLCTIWTNSR 187

RESULT 4
US-08-889-666-24
Sequence 24, Application US/08889666
Patent No. 588579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.

```

: APPLICANT: Ledbetter, Jeffrey A.
: APPLICANT: Damle, Nitin K.
: APPLICANT: Brady, William
: APPLICANT: Kiener, Peter A.
: TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 1150 Santa Monica Blvd., Suite 400
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/889,666
: FILING DATE: 08-JUL-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/375390
: FILING DATE: 18-JAN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436-350S01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 310-445-9031
: TELEFAX: 310-445-9031
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 225 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-889-666-24

Query Match          13.5%  Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%  Pred. No. 2,7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

OY 30 MEIFHNGVOIL-CKYPD--IVQOFKMLKGOIICDLTKT-KSGNTVSIKSLK---- 81
D- 30 LLYVDNNEVXSLSCRSYNLAKREFRSLYKG--VNSDYAEVCVGNFTYQOPRPNG 87
Q, 82 -FCHSOLSNNSVSFLYNLDHSHANYFCNLSTFDPFP--KYLITGXYLHIESQLC-- 136
DB 88 FNCGDNDNEVTFRMLNLDVNHHTDIYFCKEIEVMYPPPLDNEKSNGTIIHKEKHLCHA 147
OY 137 ----COLKFWLPICGCAAFVVC--ILGCIILIC--WLTKK 168
DB 148 XXXQTSRLEWPLVAVGVLGYGLTYTLCTIWTNSRR 187

RESULT 5
US-08-465-078-24
: Sequence 24, Application US/08465078
: Patent No. 5885796
: GENERAL INFORMATION:
: APPLICANT: Linsley, Peter S.
: APPLICANT: Ledbetter, Jeffrey A.
: APPLICANT: Damle, Nitin K.
: APPLICANT: Brady, William
: APPLICANT: Kiener, Peter A.
: TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
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: STREET: 1150 Santa Monica Blvd., Suite 400
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/465,078
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/375390
: FILING DATE: 18-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436-350S01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 310-445-9031
: TELEFAX: 310-445-9031
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 225 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-465-078-24

Query Match          13.5%  Score 146.5; DB 2; Length 225;
Best Local Similarity 26.2%  Pred. No. 2,7e-09;
Matches 42; Conservative 31; Mismatches 64; Indels 23; Gaps 9;

OY 30 MEIFHNGVOIL-CKYPD--IVQOFKMLKGOIICDLTKT-KSGNTVSIKSLK---- 81
D- 30 LLYVDNNEVXSLSCRSYNLAKREFRSLYKG--VNSDYAEVCVGNFTYQOPRPNG 87
OY 82 -FCHSOLSNNSVSFLYNLDHSHANYFCNLSTFDPFP--KYLITGXYLHIESQLC-- 136
DB 88 FNCGDNDNEVTFRMLNLDVNHHTDIYFCKEIEVMYPPPLDNEKSNGTIIHKEKHLCHA 147
OY 137 ----COLKFWLPICGCAAFVVC--ILGCIILIC--WLTKK 168
DB 148 XXXQTSRLEWPLVAVGVLGYGLTYTLCTIWTNSRR 187

RESULT 6
US-08-725-776-24
: Sequence 24, Application US/08725776
: Patent No. 5968510
: GENERAL INFORMATION:
: APPLICANT: Linsley, Peter S.
: APPLICANT: Ledbetter, Jeffrey A.
: APPLICANT: Damle, Nitin K.
: APPLICANT: Brady, William
: APPLICANT: Kiener, Peter A.
: TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 1150 Santa Monica Blvd., Suite 400
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-24

Query Match      13.5%  Score 146.5;  DB 2;  Length 225;
Best Local Similarity 26.2%;  Pred. No. 2.7e-09;
Matches 42;  Conservative 31;  Mismatches 64;  Indels 23;  Gaps 9;

QY 30 MFIFHNGVQIL-CRYPD--IVQGFKQMLKGGQILCDLTKT-KSGNTVSISLKL---- 81
DB 30 LLYVDNNEVXSLSCRYSYNLAKERASLYKG--VNSDVXEVCGNGNFYQPOFRPNVG 87
QY 82 -FCHSOLSNNSVSFFLYMLDHSNANYFCNLIFDPPPF--KVLITGGYLIHYESQLC-- 136
DB 88 FNCIDGNFNEFVTFRLMNLVDNHTDIYFCKIEVWYPPPYLDNEKSNGTIIHIKEKHLCHA 147
QY 137 ----COLKFWLPIGCAFAVVC--ILGCIILC--WLTTRK 168
DB 148 XXXOTSPKLFWPLVYVAGVLLCYGLLYTVTLCTIWTNSRR 187

RESULT 7
US-08-488-062-24
Sequence 24, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nithin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995

```

```

NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-062-24

Query Match      13.5%  Score 146.5;  DB 2;  Length 225;
Best Local Similarity 26.2%;  Pred. No. 2.7e-09;
Matches 42;  Conservative 31;  Mismatches 64;  Indels 23;  Gaps 9;

QY 30 MFIFHNGVQIL-CRYPD--IVQGFKQMLKGGQILCDLTKT-KSGNTVSISLKL---- 81
DB 30 LLYVDNNEVXSLSCRYSYNLAKERASLYKG--VNSDVXEVCGNGNFYQPOFRPNVG 87
QY 82 -FCHSOLSNNSVSFFLYMLDHSNANYFCNLIFDPPPF--KVLITGGYLIHYESQLC-- 136
DB 88 FNCIDGNFNEFVTFRLMNLVDNHTDIYFCKIEVWYPPPYLDNEKSNGTIIHIKEKHLCHA 147
QY 137 ----COLKFWLPIGCAFAVVC--ILGCIILC--WLTTRK 168
DB 148 XXXOTSPKLFWPLVYVAGVLLCYGLLYTVTLCTIWTNSRR 187

RESULT 8
US-08-228-208A-19
Sequence 19, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nithin K.
APPLICANT: Brady, William
APPLICANT: Wallace, Phillip M.
TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,208A
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723,617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-30US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031

```

TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 218 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-228-208A-19

Query Match
Best Local Similarity 25.7%; Pred No. 1.5e-08;
Matches 39; Conservative 24; Mismatches 61; Indels 28; Gaps 7;

Db 38 VQICKRPPD--IVQOFKMLKGGQILCDITKSGSNVSIKLF-----CHSGLSN 90
37 VSLCKRSTYLNLAKEFASLYKG--VNSDVECVGNNGFTYQPFNSNAEFNCGDFNE 94
QY 91 SVSFFLYNLDHSHANYFCNLSIFDPPF--KYLFGYLIHIESQLC---CQLKFWLP 144
D 95 TVTFRMLNHLVNHDTDYFCKIEFPNPPYLDNERSNGTIIHKEKHLCHTQSSPKLFW-- 152

QY 145 IGCAAFVVCILGC-----ILICWLTKK 168
Db 153 ---ALYVAGVLFQYGLTVALCVITNSRR 181

RESULT 9
US-08-228-208A-21
: Sequence 21, Application US/08228208A
: Patent No. 6090914
: GENERAL INFORMATION:
: APPLICANT: Linsley, Peter S.
: APPLICANT: Ledbetter, Jeffrey A.
: APPLICANT: Damle, Nitin K.
: APPLICANT: Brady, William
: APPLICANT: Wallace, Philip M.
: TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
: TITLE OF INVENTION: PROTEINS AND USES THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 1150 Santa Monica Boulevard, Suite 400
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM compatible
: SOFTWARE: FASTSEQ version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/228,208A
: FILING DATE: 15-APR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/008,898
: FILING DATE: 22-JAN-1993
: APPLICATION NUMBER: 07/723,617
: FILING DATE: 27-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436-30US01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 310 445-1140
: TELEFAX: 310 445-9031
: TELEX:
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 220 amino acids
: TYPE: amino acid

STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-228-208A-21

Query Match
Best Local Similarity 12.4%; Score 134.5; DB 3; Length 220;
Matches 44; Conservative 30; Mismatches 74; Indels 25; Gaps 7;

QY 30 MFIHNGVOILCKYPD--IVQOFKMLKGGQILCDITKSGN---TVSISLKFCH 84
Db 28 MVAVDANVNIKCYSTNLSRFRASLHKLDSAVCVYGNISQQLQVYSKTFNCD 87
QY 85 SOLSNYSFPLYNLDHSHANYFCNLSIFDPPF--KYLFGYLIHIESQLCQLKFW 142
Db 88 GKLGNESVTFYLNQNDYFCKIEVMPYLDNERSNGTIIHVKGHLCPSPPLF- 146

QY 143 LPICAAFFVVCILGCILIC-----WLTKKYSVHDPNGEYFM 183
Db 147 -GSPSKPFWLVVGVGLACSLTYVAFIFVRSKR-SRLH--SDYMM 194

RESULT 10
US-08-505-058-3
: Sequence 3, Application US/08505058
: Patent No. 5773253
: GENERAL INFORMATION:
: APPLICANT: Linsley, Peter S.
: APPLICANT: Ledbetter, Jeffrey A.
: APPLICANT: Peach, Robert
: TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 1150 Santa Monica Blvd., Suite 400
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/505,058
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/228,208
: FILING DATE: 15-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Adriano, Sarah B.
: REGISTRATION NUMBER: 34,470
: REFERENCE/DOCKET NUMBER: 30436-30US11
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 310-445-1140
: TELEFAX: 310-445-9031
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 225 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-505-058-3

Query Match
Best Local Similarity 12.4%; Score 134; DB 1; Length 225;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;

QY 11 FCLRKVLVTEIGNSANYEMFIHNGVOILCKYPD--IVQOFKMLKGGQILCDITKT 68


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Db      12 FXSVQVTEENKILVQSPDLTVDSNEVYSLSCRSYNNLAKEFASLYKG--VNSDXEY 6
Oy      69 -KGSQNTWYSIKSLKF-----CHSOLSNNSVSFFPLYNDHSHANYPCFLSTFDDPPF--K 120
Db      70 CVGNGNFFLYQOPFRSNAEFNCDGPDENFTVTFRLMLNLHVNTDILYFKIEPMYPPLDN 129
Oy      121 VTLRGVLIHYESOLC-----COLKRWLPICGAAPVYVCLIC-----LLIOWLT 165
Db      130 ERSNQTIIHIKEKHLCHTXXXQSSPKLFW-----ALYVAGVLCYGLTVLVALCVIWTN 184
Oy      166 KKK 168
Db      185 SRR 187

RESULT 11
US-08-459-818-23
Sequence 23, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fastseq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-23

Query Match 12.4%: Score 134; DB 2; Length 225;
Best Local Similarity 23.0%: Pred. No. 8e-08;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps

Oy      11 FCLRLKVLGTGINSANVEMPIFHNGVOILCKYPD--IYQPFKMLLKGQILCDLTKT 68
Db      12 FFXSVQVTEENKILVQSPDLTVDSNEVYSLSCRSYNNLAKEFASLYKG--VNSDXEY 69
Oy      69 -KGSQNTWYSIKSLKF-----CHSOLSNNSVSFFPLYNDHSHANYPCFLSTFDDPPF--K 120
Db      70 CVGNGNFFLYQOPFRSNAEFNCDGPDENFTVTFRLMLNLHVNTDILYFKIEPMYPPLDN 129
Oy      121 VTLRGVLIHYESOLC-----COLKRWLPICGAAPVYVCLIC-----LLIOWLT 165
Db      130 ERSNQTIIHIKEKHLCHTXXXQSSPKLFW-----ALYVAGVLCYGLTVLVALCVIWTN 184
Oy      166 KKK 168
Db      185 SRR 187

130 ERSNQTIIHIKEKHLCHTXXXQSSPKLFW-----ALYVAGVLCYGLTVLVALCVIWTN 184

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OY      166 KKK 168
DB      185 SRR 187

RESULT 12
US-08-889-666-23
; Sequence 23, Application US/088989666
; Patent No. 5885579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienert, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pctel In Release #1.0, Version #1.30
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-Jul-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-Jan-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-23

Query Match          12.4%; Score 134; DB 2; Length 225;
Best Local Similarity 23.0%; Pred. No. 8e-08;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;
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RESULT 13
US-08-465-078-23
Sequence 23, Application US/08465078
Patent No. 5885796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-350S01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-9031
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-23

Query Match
Best local Similarity 23.0%; Pred. No. 88-08; Length 225;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;

DB 11 FCLRIKVLGEINGSANYEMFIFHNGVOILCKYPD--IVQOFKQMLKGGQILCDLTKT 68
DB 12 FFXSVQVTEKNIKLVKOSPLLYVDSNEYXSLSCRYTNLAKERASLYKG--VNSDVXEV 69
DB 69 -KSGNTVSIKSLKF-----CHSOLSNNSVSFLYVLDHSHANYFCNLSIDPPPF--K 120
DB 70 CVDGNGNTYQOPFRSNAEFNCDDGDFDNETVTFRLMNLVHNNHTDIYFCKIEFMVPPPYLDN 129
DB 121 VTLTGYLHYESQLC-----COLKFWLPICGAFVYVCILGC-----ILICWLT 165
DB 130 ERSNGTIIHKEKHLCHTXXXSPLFW-----ALYVAGVLFYGLLVVALCVIMTN 184
DB 166 KKK 168
DB 185 SRR 187

RESULT 14
US-08-725-776-23
Sequence 23, Application US/08725776

Patent No. 5968510
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-350S01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-9031
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-23

Query Match
Best local Similarity 23.0%; Pred. No. 88-08; Length 225;
Matches 42; Conservative 32; Mismatches 77; Indels 32; Gaps 8;

DB 11 FCLRIKVLGEINGSANYEMFIFHNGVOILCKYPD--IVQOFKQMLKGGQILCDLTKT 68
DB 12 FFXSVQVTEKNIKLVKOSPLLYVDSNEYXSLSCRYTNLAKERASLYKG--VNSDVXEV 69
DB 69 -KSGNTVSIKSLKF-----CHSOLSNNSVSFLYVLDHSHANYFCNLSIDPPPF--K 120
DB 70 CVDGNGNTYQOPFRSNAEFNCDDGDFDNETVTFRLMNLVHNNHTDIYFCKIEFMVPPPYLDN 129
DB 121 VTLTGYLHYESQLC-----COLKFWLPICGAFVYVCILGC-----ILICWLT 165
DB 130 ERSNGTIIHKEKHLCHTXXXSPLFW-----ALYVAGVLFYGLLVVALCVIMTN 184
DB 166 KKK 168
DB 185 SRR 187

RESULT 15
US-08-488-062-23
Sequence 23, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.

Mon Oct 21 07:51:55 2002

us-09-823-307c-2.rai

Page 8

APPLICANT: Brady, William
 APPLICANT: Kienery, Peter A.
 TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant & Gould
 STREET: 1150 Santa Monica Blvd., Suite 400
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,062
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/375390
 FILING DATE: 18-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Adriano, Sarah B.
 REGISTRATION NUMBER: 34,470
 REFERENCE/DOCKET NUMBER: 30436-35US01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 INFORMATION CHAR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 225 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-062-23

Matches 44; Conservative 30; Mismatches 74; Indels 25; Gaps 7;

QY 30 MEIFNGGVOLICKYPD--IVQOFKMOCLKGQILCDLTKRKGSGN---TVSIKSLKFC 84
 DB 28 MLVAYDNAVNLSCKSYNLFSEFRASLHKGLDSAVECVYGYNSOOLQYXKTEFNCD 87
 QY 85 SOLSNNSVSEFLYNLDHSHANYFCNLSIFDPPF--KVLITGGLHIYESQLCCOLKFW 142
 DB 88 GKLGNESVTFYLOMLVYNQTDIYFKIEVMYPPYLDNEKSNGTIIHKCKHLCPSPFLF- 146
 QY 143 LPICGAFAVVCIIIGCIIIC-----WLTKKRYSSVHDPNGEYMF 183
 DB 147 -PGSPKPFMALVYVGVYACYSILVTAFCIEFMRSKR-SRLH---SDYNNM 194

RESULT 14
 ID Q9BDN5 PRELIMINARY; PRT; 220 AA.
 AC Q9BDN5; 01-JUN-2001 (TREMBlrel. 17, Created)
 DE 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CD28 PROTEIN.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecidae.
 NC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 RL EMBL: AF344842; AAK37601.1; --
 DR HSSP: P16410; 1AHL
 DR InterPro: IPR003600; IG-like.
 DR SMART: SM00410; IG-like; 1
 SO SEQUENCE 220 AA; 25117 MW; 13BD03F7D937388F CRC64;

Query Match 12.5%; Score 130.5; DB 6; Length 220;
 Best Local Similarity 25.4%; Pred. No. 1.2e-06;
 Matches 44; Conservative 30; Mismatches 74; Indels 25; Gaps 7;

QY 30 MEIFNGGVOLICKYPD--IVQOFKMOCLKGQILCDLTKRKGSGN---TVSIKSLKFC 84
 DB 28 MLVAYDNAVNLSCKSYNLFSEFRASLHKGLDSAVECVYGYNSOOLQYXKTEFNCD 87
 QY 85 SOLSNNSVSEFLYNLDHSHANYFCNLSIFDPPF--KVLITGGLHIYESQLCCOLKFW 142
 DB 88 GKLGNESVTFYLOMLVYNQTDIYFKIEVMYPPYLDNEKSNGTIIHKCKHLCPSPFLF- 146
 QY 143 LPICGAFAVVCIIIGCIIIC-----WLTKKRYSSVHDPNGEYMF 183
 DB 147 -PGSPKPFMALVYVGVYACYSILVTAFCIEFMRSKR-SRLH---SDYNNM 194

RESULT 15
 ID Q9BDM6 PRELIMINARY; PRT; 220 AA.
 AC Q9BDM6; 01-JUN-2001 (TREMBlrel. 17, Created)
 DE 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CD28 PROTEIN PRECURSOR
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NC NCBI_TaxID=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 RL EMBL: AF344842; AAK37601.1; --
 DR HSSP: P16410; 1AHL
 DR InterPro: IPR003600; IG-like.
 DR SMART: SM00410; IG-like; 1
 DR Signal.
 KW SIGNAL.
 FT SIGNAL 1 18
 FT VARIANT 34 34
 FT VARIANT 70 70
 FT VARIANT 71 71
 FT VARIANT 83 83
 FT VARIANT 122 122
 FT VARIANT 175 175
 FT VARIANT 209 209
 SQ SEQUENCE 220 AA; 25125 MW; 03776183006AE042 CRC64;

Query Match 12.1%; Score 130.5; DB 6; Length 220;
 Best Local Similarity 25.4%; Pred. No. 4.1e-06;
 Matches 44; Conservative 28; Mismatches 76; Indels 25; Gaps 7;

QY 30 MEIFNGGVOLICKYPD--IVQOFKMOCLKGQILCDLTKRKGSGN---TVSIKSLKFC 84
 DB 28 MLVAYDNAVNLSCKSYNLFSEFRASLHKGLDSAVECVYGYNSOOLQYXKTEFNCD 87
 QY 85 SOLSNNSVSEFLYNLDHSHANYFCNLSIFDPPF--KVLITGGLHIYESQLCCOLKFW 142
 DB 88 GKLGNESVTFYLOMLVYNQTDIYFKIEVMYPPYLDNEKSNGTIIHKCKHLCPSPFLF- 146
 QY 143 LPICGAFAVVCIIIGCIIIC-----WLTKKRYSSVHDPNGEYMF 183
 DB 147 -PGSPKPFMALVYVGVYACYSILVTAFCIEFMRSKR-SRLH---SDYNNM 194

Search completed: October 21, 2002, 07:48:15
 Job time : 32 secs

Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
32 IFHNGVQIILCKRPD--IVQGFKMLLKGGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86	27.2%	140.5	DB 6	221	46	26	76	21	
31 VVYNNEVNLSCRTYTNLFSEKFPASLYKGDVSAVECVVANGNSHOPFVSTGFCDDGK 90	27.2%	140.5	DB 6	221	46	26	76	21	
87 LSNNSVSEFLYNLDHSHANYPCNLSIEDPPPP--KVTLTGAYLHIYESQLC-----C 137	27.2%	140.5	DB 6	221	46	26	76	21	
91 LGNETVTFYRNLFVNQTDIYFKIEVMPPPYIGNEKSNGTIIHVEKHLCPDELPFDS 150	27.2%	140.5	DB 6	221	46	26	76	21	
138 QLKFM-LPIGCAAFVYVVCILGCLIC--WLTKKTYSSSVHPDNGEYFM 183	27.2%	140.5	DB 6	221	46	26	76	21	
151 SKPFMALVYVGAVLVFYSLLVVALCAVYIKSK--SSRI--LQSDYMM 195	27.2%	140.5	DB 6	221	46	26	76	21	
Query Match	Best Local Similarity	Score	DB	Length	Matches <td>Conservative<td>Mismatches<td>Indels<td>Gaps</td></td></td></td>	Conservative <td>Mismatches<td>Indels<td>Gaps</td></td></td>	Mismatches <td>Indels<td>Gaps</td></td>	Indels <td>Gaps</td>	Gaps
32 IFHNGVQIILCKRPD--IVQGFKMLLKGGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86	27.2%	140.5	DB 6	221	46	26	76	21	
31 VVYNNEVNLSCRTYTNLFSEKFPASLYKGDVSAVECVVANGNSHOPFVSTGFCDDGK 90	27.2%	140.5	DB 6	221	46	26	76	21	
87 LSNNSVSEFLYNLDHSHANYPCNLSIEDPPPP--KVTLTGAYLHIYESQLC-----C 137	27.2%	140.5	DB 6	221	46	26	76	21	
91 LGNETVTFYRNLFVNQTDIYFKIEVMPPPYIGNEKSNGTIIHVEKHLCPDELPFDS 150	27.2%	140.5	DB 6	221	46	26	76	21	
138 QLKFM-LPIGCAAFVYVVCILGCLIC--WLTKKTYSSSVHPDNGEYFM 183	27.2%	140.5	DB 6	221	46	26	76	21	
151 SKPFMALVYVGAVLVFYSLLVVALCAVYIKSK--SSRI--LQSDYMM 195	27.2%	140.5	DB 6	221	46	26	76	21	

DN 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE CELL SURFACE PROTEIN (FRAGMENT).
 GN CD28.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEAGLE.
 RX MEDLINE=94222451; PubMed=8168859;
 RA Pastori R.L., Milde K.F., Alexandro R.;
 RT "Molecular cloning of the dog homologue of the lymphocyte antigen
 CD28.";
 RL Immunogenetics 39:373-373(1994).
 DR EMBL, L22178; AA51453.1;
 DR InterPro: IP003600; IG_1like.
 DR SMART: SM00410; IG_1like; 1.
 FT NON_TER
 FT NON_TER 1
 FT SEQUENCE 173 AA; 19770 MW; 76265AE40931C1EA CRC64;
 SO
 Query Match 12.9%; Score 139.5; DB 6; Length 173;
 Best Local Similarity 26.8%; Pred. No. 3.3e-07;
 Matches 41; Conservative 24; Mismatches 71; Indels 17; Gaps 7.
 Oy 32 IFHNGVOILCKRPD--IVQFKNMOLLKGGQILCDLTFTKGS--SGNVTSIKSLKF-CHSQ 86
 Db 12 VVVYNNENVLCKCTYTNLFSKEFRASIVYGVSAVCECVANNYSHOPQFYSNGFDGCK 71
 Oy 87 LSNNSVEFFLYNLDHSHANYVCNLSIFDPPEF--KVLITGGLYHIESOLC-----C 137
 Db 72 LGNETVTFYLRNLFVNGQDITFYCKILEWVPPYIGNEKSNCTIIHVKELKCPDELFPDS 131
 Oy 138 QLKPM-LPTGCAAFVYVVCITGLICLC-WLRKK 167
 Db 132 SKPPMALVVYGAIVLFPYSLVYVALCAWIKSK 164
 RESULT 13
 O9BDM8 PRELIMINARY; PRT. 220 AA.
 AC O9BDM8;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 17, Last annotation update)
 DE C288 PROTEIN PRECURSOR.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/FasLliland and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF544852; AAK37612.1; .
 DR HSSP: P16410; IAH1
 DR InterPro: IP003600; IG_1like.
 DR SMART: SM00410; IG_1like; 1.
 KN Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT SIGNAL 215 215 S.F.
 FT VARIANT 220 AA; 24966 MW; 965f6d54DAF1AF0A CRC64;
 SO
 Query Match 12.6%; Score 136.5; DB 6; Length 220;
 Best Local Similarity 25.4%; Pred. No. 9.2e-07;

```

Db 131 GTVHVKNENNICPGVSPSPKPFMTLVFSGVLGYLSTLMCLCYLMTKRQRTRL-L 188
QY 177 NGEYFM 183
Db 189 OSDYMM 195

RESULT 7
ID 09N214 PRELIMINARY; PRT; 221 AA.
AC 09N214:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CD28.
GN CD28.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20094001; PubMed=10630305;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell
RT antigen CD28 homologue.";
RL Immunogenetics 50:369-370(1999).
DR EMBL; AB025316; BAA92349.1; -
DR InterPro; IPR003600; IG_1like.
DR SMART; SM00410; IG_1like.1;
SO SEQUENCE 221 AA; 25283 MW; B17B76C5BA18DCB CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;
Best Local Similarity 28.3%; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGVOILCKYPD--IVQOFKMLKGGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVNLSCRYTHNLFSEKFRASLYKGDSAVECVVANGNSHQPFYSTGFDDCK 90

QY 87 LSNNVSFFLYNLDSHANYFCNLSTFDPPPF--KYLGLGYLHYESQLC-CQLK--- 140
Db 91 LGNETVTFYLNLFVNQTDIFYFCKIEVWPPPIIDNEKSNGTIIVHKEKHLCPAQLSPES 150

QY 141 ---FWLPICGAFFVVCILG-----CILICWLTKK 168
Db 151 SKPEW-----ALVYVGILGFYSILATVALGACWMTKR 184

RESULT 8
ID 002757 PRELIMINARY; PRT; 221 AA.
AC 002757:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;

[1]
RP SEQUENCE FROM N.A.
RA Hash S.M., Carpio M.R., Collisson E.W.;
RT "Felis catus t-cell specific surface glycoprotein CD28.";
RL Thesis (1996); Veterinary Pathobiology, Texas A&M Univ.
DR EMBL; U57754; AAB53574.1; -
DR InterPro; IPR003600; IG_1like.
DR SMART; SM00410; IG_1like.1;
SO SEQUENCE 221 AA; 25317 MW; 5B71717E46AE5E3 CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;

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Best Local Similarity 28.3%; Pred. No. 9.8e-08;
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGVOILCKYPD--IVQOFKMLKGGQILCDLTKTG--SGNTVSIKSLKF-CHSQ 86
Db 31 VVYNNEVNLSCRYTHNLFSEKFRASLYKGDSAVECVVANGNSHQPFYSTGFDDCK 90

QY 87 LSNNVSFFLYNLDSHANYFCNLSTFDPPPF--KYLGLGYLHYESQLC-CQLK--- 140
Db 91 LGNETVTFYLNLFVNQTDIFYFCKIEVWPPPIIDNEKSNGTIIVHKEKHLCPAQLSPES 150

QY 141 ---FWLPICGAFFVVCILG-----CILICWLTKK 168
Db 151 SKPEW-----ALVYVGILGFYSILATVALGACWMTKR 184

RESULT 9
ID 097630 PRELIMINARY; PRT; 219 AA.
AC 097630:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.
GN CD28.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprine; Ovis.
NCBI_TaxID=9940;

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309828; PubMed=10380709;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
DR EMBL; AF092739; AAD04379.1; -
DR InterPro; IPR003600; IG_1like.
DR SMART; SM00410; IG_1like.1;
SO SEQUENCE 219 AA; 25158 MW; D50AD339E5BC2327 CRC64;

Query Match 13.4%; Score 145; DB 6; Length 219;
Best Local Similarity 23.5%; Pred. No. 1.1e-07;
Matches 40; Conservative 35; Mismatches 75; Indels 20; Gaps 8;

QY 30 IFHNGVOILCKYPD--IVQOFKMLKGGQILCDLTKTG--GNTVSIKSLKF-CHS 85
Db 28 MLVYNDNEVNLSCRYTYNLFSEKFRASLYKGDSAVECAVNGHSHPLDSTNKEFNCTV 87

QY 86 QLSNVSFFLYNLDSHANYFCNLSTFDPPPF--KYLGLGYLHYESQLC----- 136
Db 88 KVGNETVTFYLDLDLYVNQTDIFYFCKLELYPPPIIDNEKSNGTIIVHKEKHLCPSPSE 147

QY 137 CQLKEWLPF---GCAAFVVCILGCIILCWLTKKRYSSVHPDNGEYFM 183
Db 148 SSKPEWALVYVNGVLYFVSLATVALGACWMTKR--NRMH--OSDYMM 193

RESULT 10
ID 09GKP3 PRELIMINARY; PRT; 221 AA.
AC 09GKP3:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE COSTIMULATORY MOLECULE B7 RECEPTOR CD28.
GN CD28.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;

[1]
RP SEQUENCE FROM N.A.

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QY 64 DLRTKSGNTVAIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 122
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 ELRTKSGNAVASIKNPMCLYHLNNSVSFFLNPNDSOGSYFCLSLIFDPPPEOEN 123
QY 123 LTGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 182
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 LSGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 183
QY 183 MRAVNTAKKSRLDVT 198
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 MAAVNTAKKSRLAGMT 199

RESULT 4
QYRTT 7 PRELIMINARY: PRT: 200 AA.
ID 09RTT7
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
D. RECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat Ailim/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL: AB023134; BAA82128.1;
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22529 MW; 0A74C3581F129D4 CRC64;

Query Match 64.8%; Score 701; DB 11; Length 200;
Best Local Similarity 67.9%; Pred. No. 5.4e-68;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

QY 7 YF---FLECLRIYVLGEINGSANYEMFIHNGGVOLICKYPIYQOFKMLKGGOLIC 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 YFSCVFYFCLIKLIGELNDLANHMFSPHDGVOISCNFETVOQLKMLFKDREVLC 63
QY 64 DLRTKSGNTVAIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 122
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 DLRTKSGNTVAIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 122
QY 123 LTGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 182
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 LSGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 183
QY 183 MRAVNTAKKSRLDVT 198
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 MAAVNTAKKSRLAGMT 199

RESULT 5
QYRTT 9 PRELIMINARY: PRT: 216 AA.
ID 09WVR9
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
D. RECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SPLEEN;
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Tamatani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat Ailim/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL: AB023133; BAA82127.1;
KM SIGNAL.
FT SIGNAL.
SQ SEQUENCE 216 AA; 24260 MW; 772E01320982B15A CRC64;

Query Match 64.3%; Score 696; DB 11; Length 216;
Best Local Similarity 68.8%; Pred. No. 2.1e-67;
Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;

QY 7 YF---FLECLRIYVLGEINGSANYEMFIHNGGVOLICKYPIYQOFKMLKGGOLIC 63
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 YFSCVFYFCLIKLIGELNDLANHMFSPHDGVOISCNFETVOQLKMLFKDREVLC 63
QY 64 DLRTKSGNTVAIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 122
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 DLRTKSGNTVAIKSLKFCCHSOLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 122
QY 123 LTGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 182
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 LSGGYLIHYESOLCCOLKFWLPICGAFFVYVLCILICMLTKRRYSSVHDPMGEYWF 183
QY 183 MRAVNTAKKSRL 194
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 MAAVNTAKKSRL 195

RESULT 6
QYRTT 6 PRELIMINARY: PRT: 221 AA.
ID 09JLV4
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CD28 ANTIGEN.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX Lu M., Yang D., Kemper T., Maier A., Rogendorf M.;
RT "Molecular characterization of woodchuck CD28 and cytotoxic T-
RT lymphocyte associated antigen 4 (CTLA-4).";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF130427; AAF36501.1;
DR InterPro: IPR003600; Ig-like.
DR SMART: SM00410; Ig-like; 1.
SQ SEQUENCE 221 AA; 25594 MW; B29D32E987CE51D1 CRC64;

Query Match 13.5%; Score 146.5; DB 11; Length 221;
Best Local Similarity 23.0%; Pred. No. 7.6e-08;
Matches 43; Conservative 36; Mismatches 71; Indels 37; Gaps 7;

QY 14 RIKVLTEINGSANYEMFIHNGGVOLICKYPIYQOFKMLKGGOLICDLTKRSGSN 73
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 RLEYNNNEVLSCKRYNYLFS-----KEFRASLYKGVDSAVEYCVVNGNFS 74
QY 74 TVSIKSLK-----CHQLSNNSVSFFLYNLDHSHANYFCNLSIFDPPPEKV-T 124
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 -----HQLQFYSHRGFNCDKLSTNETYTFYLRNLVYVQNTDYCKIEVMPRPYLDNEKSN 130
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 GYLIHYESOLCCOL-----KFW-LPIGCAFFVYVLCILICMLTKRRYSSVNDP 176
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 20 Seconds

(without alignments)
956.089 Million cell updates/sec

Title: US-09-823-307C-2

Sequence: 1 MKSGLMYFFLFCLRIKIVLNG.....YMFMAVNTAKSRLLDTVL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Tc: number of hits satisfying chosen parameters: 283138

Min. num DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR-71:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	2	S78540
2	701	64.8	200	2	JC7397
3	684	64.3	216	2	JC7396
4	152	14.0	216	2	S24113
5	150.5	13.9	221	2	I46889
6	139.5	12.9	173	2	I46197
7	139.5	12.9	220	1	RWH028
8	138	12.8	218	2	A43523
9	103.5	9.6	268	2	T18986
10	97	9.0	221	2	S25168
11	91.5	8.5	383	2	T21946
12	87	8.0	330	2	A40071
13	87	8.0	330	2	I49660
14	87	8.0	563	2	T33479
15	86.5	8.0	223	2	A29063
16	86	7.9	223	2	T09536
17	84	7.8	283	1	FCMSG1
18	84	7.8	285	1	A269440
19	83.5	7.7	186	2	S08614
20	82.5	7.6	248	1	QOBE4L
21	81	7.5	276	2	S20690
22	81	7.5	680	2	JCS695
23	81	7.5	1584	2	S57161
24	80.5	7.4	247	2	D90028
25	80.5	7.4	635	2	JCS696
26	78	7.2	231	2	T23136
27	77.5	7.2	80	2	F86027
28	77.5	7.2	220	2	A48581
29	77.5	7.2	1070	2	JC4593

ALIGNMENTS

30	77	7.1	338	2	T34364	hypothetical prote
31	77	7.1	2104	2	D91286	hypothetical prote
32	77	7.1	2104	2	H86127	hypothetical prote
33	76.5	7.1	223	2	I46696	CTLA-4 precursor -
34	76.5	7.1	323	2	S06946	Fc gamma (IgG) rec
35	76.5	7.1	1237	2	A54080	protein-tyrosine-p
36	76	7.0	301	2	I54209	hypothetical prote
37	76	7.0	317	2	JU0118	Fc gamma (IgG) rec
38	76	7.0	546	2	S52053	cytochrome-c oxida
39	75.5	7.0	261	2	S29360	Fc gamma (IgG) rec
40	75.5	7.0	277	2	T21330	hypothetical prote
41	75.5	7.0	2135	2	T14602	variant-specific s
42	75	6.9	418	2	AD3417	transporter, mem s
43	75	6.9	1132	1	Q8BPL	host specificity p
44	74.5	6.9	201	2	G90134	hypothetical prote
45	74.5	6.9	235	2	I50610	T-cell surface gly

RESULT 1

S78540 Inducible T-cell co-stimulator ICOS precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Mar-1999 #sequence-revision 05-Mar-1999 #text-change 07-May-1999

C:Accession: S78540; S78748; S78749

R:Kloczek, R.

submitted to the Protein Sequence Database, June 1998

A:Accession number: S78540

A:Molecule type: mRNA

A:Residues: 1-199 <KRO>

A:Experimental source: cell line MOLT-4V

A:File: ICOS is an inducible T-cell co-stimulator structurally and functionally rela

A:Reference number: S78748; MUID:99127892

A:Accession: S78748

A:Molecule type: mRNA

A:Residues: 1-199 <HUT1>

A:Experimental source: cell line MOLT-4V

A:Accession: S78749

A:Molecule type: protein

A:Residues: X, 193-198 <HUT2>

A:Experimental source: cell line MOLT-4V

C:Complex: homodimer

C:Superfamily: Immunoglobulin homology

C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein

F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG>

F:21-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT>

F:21-138/Domain: extracellular #status predicted <EXT>

F:139-164/Domain: immunoglobulin homology <IMM>

F:165-199/Domain: transmembrane #status predicted <TM>

F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1082; DB 2; Length 199;

Best Local Similarity 100.0%; Pred. No. 3, 1e-97; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKSGLMYFFLFCLRIKIVLNGSANYEMFIHNGVQILCKYPDVOQFMKQLLGQ	60
Db	1	MKSGLMYFFLFCLRIKIVLNGSANYEMFIHNGVQILCKYPDVOQFMKQLLGQ	60
Qy	61	ILCDLTKRSGNIVSKLKFCHSQSLNSNSVFFLVNLDHSHANYFCNLSIFDPPFK	120
Db	61	ILCDLTKRSGNIVSKLKFCHSQSLNSNSVFFLVNLDHSHANYFCNLSIFDPPFK	120
Qy	121	VTLLGGYHIVESQCLQKFMPLPGCAAFVYVVICILCIIICMTKKKSSVHPDNGEY	180
Db	121	VTLLGGYHIVESQCLQKFMPLPGCAAFVYVVICILCIIICMTKKKSSVHPDNGEY	180

[illegible]

Db 87 CDGDEDFNEFVRLNHLVHNTDIYFCIEFMPPEPPLDNRSGRTIHKKEHLCHTOS 146
 Oy 137 COLKFWLPGCAAFVYVILGC-----ILICWLTKKK 168
 Db 147 SPKLFV-----ALVYVAGVLCFYGLLVALCVATWTSNR 181

RESULT 9

hypothetical protein C06B3.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: J18986

R:Pericy, C.
 Submitted to the EMBL Data Library, July 1996

A:Reference number: Z19056
 A:Accession: J18986
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Cross-references: EMBL:Z77652; PIDN:CAH01120.1; GSPDB:GN00023; CESP:C06B3.11
 A:Experimental source: clone C06B3
 A:Gene: CESP:C06B3.11

A:Map position: 5
 A:Introns: 21/3; 75/2; 124/2; 150/1; 204/3; 239/2; 274/1; 330/3; 366/3; 407/1; 441/2; 542

Query Match 9.6%; Score 103.5; DB 2; Length 988;
 Best Local Similarity 23.0%; Pred. No. 0.079;

Matches 55; Conservative 29; Mismatches 74; Indels 81; Gaps 12;

Oy 6 WYFLFCRLIVLT-----GEINGSANVEMFIFNNG-----VOILCK 43
 Db 324 WYCFASFMLLTVMILPFESACGSPDYLFAPRSCGCPKWHITOPFLASYFWIVPVCC 383
 Oy 44 YPDIVQOFKMOY--LKGQIICDLTKTSGNVT-----IKSEKFSHLSNNS 91
 Db 384 VLNIILFHMSLKSKKNOM-----SONSASARQERLLIQLSLTFLISHEI 434
 Oy 92 VSF-----ELYNLDHSHANYF-----CNLSIFPPPEFKYL--NGYLHIYES 134
 Db 435 ASFTLELFPFIETFDNGTFLIFISHDVYSMFFMTDPSVHLQTKRL--IDPS 493
 Oy 135 L---CCQLKFWLPICGAFFVYVILGCT-----LICWLTKKKYSSVHDNGEYFM 183
 Db 494 LEIKSCKEPDLPVYVYIYLMACISIGCEVEFOSDIIYFMKR-----ATMM 542

RESULT 10

525168
 CHT28 protein - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: J50619; S25168

R:Young, J.R.; Davidson, T.F.; Tregaskes, C.A.; Renzie, M.C.; Valino, O.
 J. Immunol. 152, 3848-3851, 1994

A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A:Reference number: J50619; MUID:94194147
 A:Accession: J50619

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-221 <Y02>
 A:Cross-references: EMBL:X67915; NID:963221; PIDN:CAA48114.1; PID:963222

C:Family: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match 9.0%; Score 97; DB 2; Length 221;
 Best Local Similarity 22.8%; Pred. No. 0.066; 78; Indels 34; Gaps 9;
 Matches 41; Conservative 27; Mismatches 78; Indels 34; Gaps 9;
 Oy 26 ANYEFLPHNGVOILCKYP--DIVQOFKMOILKGO-----ILCDLTKKSGSNTVS 76

Db 24 AORPLLIANRATATVCGTYNGTGEFRASLHKGTDSAVEGCFISNMKINSNK-- 81
 Oy 77 IKSLKF--CHSOLSNNSFFLYNLDHSHANYPCNLSTFPP--FKVTLGGLHYES 133
 Db 82 ----EFNCRGHDHDKVIFNLMNMSASOTDIYFCKIEAMPPPVYVKEKNGVIVHRE 137
 Oy 134 OLCCO-----LKFPLPI--GCAAFVYVILGCLICWLTKK--KYSSVHDNGEYFM 183
 Db 138 PIQTOEPESATISVWYVAVVGLGFIYSLITAVFIITRQSKRRYKOS-----DYM 191

RESULT 11

hypothetical protein F38B2.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: J21946

R:Kershaw, J.
 Submitted to the EMBL Data Library, July 1995

A:Reference number: Z19492
 A:Accession: J21946
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-383 <W1L>

A:Cross-references: EMBL:Z50045; PIDN:CAA90363.1; GSPDB:GN00028; CESP:F38B2.3
 A:Experimental source: clone F38B2
 A:Gene: CESP:F38B2.3

A:Map position: X
 A:Introns: 21/1; 52/1; 135/2; 184/1; 226/2; 260/2; 299/1; 359/2

Query Match 8.5%; Score 91.5; DB 2; Length 383;
 Best Local Similarity 23.6%; Pred. No. 0.41;

Matches 38; Conservative 23; Mismatches 51; Indels 49; Gaps 8;

Oy 43 YPDIVQOFKMOILKGOIICD--LTKTSGNVTSTKSLFCHSOLSNNSVFFYVND 100
 Db 240 KYHDFIK-----LYDGNSTDPITRISGOENVYTN-----STSNILFFFLMD 284
 Oy 101 HS-----HANYPCNLSIFDPPEFKYLTGGLYHIYESOLCQKFWLPICGAFFV 154
 Db 285 ESNCKGKHANY-----ARMTIDHILGETH-----WYLVCAVFLTY 324
 Oy 155 ILGCLICWLTKK--KYSSVHDNGEYFMRA--VNTA 189
 Db 325 MIAGYIVFVIRKENHKOLESIMPTISSSSEAGSSINIA 365

RESULT 12

A40071
 Fc gamma (Ilg) receptor II (low affinity) beta (splice form 1) precursor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 23-Jul-1999
 C:Accession: A40071; A60761; S29361

R:Hogarth, P.M.; Willett, E.; Hulet, M.D.; Bonnerot, C.; Even, J.; Fildman, W.H.; McI
 J. Immunol. 146, 369-376, 1991

A:Title: Structure of the mouse betaFc gamma receptor II gene.
 A:Reference number: A40071; MUID:91079576
 A:Accession: A40071

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-330 <HOG>

A:Cross-references: GB:M63284; NID:9192161; PIDN:AAA37289.1; PID:9192163
 R:Rah, M.; Quelch, K.; Deacon, N.J.; McKenzie, I.F.C.; Hogarth, P.M.
 Immunogenetics 31, 202-206, 1990

A:Title: Identification of the mouse beta Fc gamma II polymorphism by direct sequencin
 A:Reference number: A60761; MUID:90202030

A:Accession: A60761
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-146, P, 146-189, Q, 191-298, P, 300-330 <LAH>
 A:Cross-references: GB:M31312; NID:9193260; PIDN:AAA37610.1; PID:9387155
 R:Raveloch, J.V.; Luster, A.D.; Weinstein, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.

Science 234, 718-725, 1986
 A>Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc r
 A/Reference number: S29360; MUID:87042761
 A/Accession: S29361
 A/Status: Preliminary
 A/Molecule type: mRNA
 A/Residues: 1-269, 'L', 271, 'A', 'CO', 276, 'RA', 279-330 <RAV>
 A/Cross-references: EMBL:M16367; NID:g193256; PIRN:AAA37608.1; PID:g309230
 C/Superfamily: Fc gamma receptor III; Immunoglobulin homology
 C/Keywords: Immunoglobulin receptor
 F:1-29/Domain: signal sequence
 F:50-101/Domain: immunoglobulin homology <IMM1>
 F:131-184/Domain: immunoglobulin homology <IMM2>

Query Match 8.0%; Score 87; DB 2; Length 330;
 Best Local Similarity 20.4%; Pred. No. 0.95;

Matches 44; Conservative 29; Mismatches 53; Indels 90; Gaps 11;

QY 33 FHNG---GVOILCKPYDVOQFMOLKGGQILDLTKGK-----71
 D 71 FHNGRSIRSOVASY---TFKATVNDSEYRCOMEQTRLSQVLDGVISDWLLQTPQ 125
 QY 72 ---GNVSIKSLKFCQSOLSN--NSVSFF-----LYNLDHSNANYE 108
 D 126 LVFLBETITLR---CHSWRNKLNRISEFHNKSVRYHHYSSNFSIPKRNHSHSGDY 181
 QY 109 CNLS---IFDPPPKVTLTGGLHYESOLCCQKFWLPI-----GCAAFVVCIL 156
 D 182 CKGSLGRTHOSKPVITVQGP-----KSSRSPLVLTIVAAYVGIIVAIL 230
 QY 157 GCILICMLTKKKYSSVHDPN-----GEY 180
 D 231 --VSLVYLKKQVPALPGNPDHREMGETLPEEYGEY 264

RESULT 13

149660
 Fc-gamma-1/gamma-2b receptor precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C/Accession: I49660
 R/Hogarth, P.M.; Hibbs, M.L.; Bonadonna, L.; Scott, B.M.; Wlort, E.; Pietersz, G.A.; Mc
 Immunogenetics 26, 161-168, 1987
 A>Title: The mouse Fc receptor for IgG (Ly-17): Molecular cloning and specificity.
 A/Reference number: I49660; MUID:87306729
 A/Accession: I49660
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-330 <RES>
 A/Cross-references: GB:M17515; NID:g193254; PIDN:AAA37607.1; PID:g309229
 C/Superfamily: Fc gamma receptor III; Immunoglobulin homology
 C/Keywords: Immunoglobulin receptor
 F:131-184/Domain: immunoglobulin homology <IMM>

Query Match 8.0%; Score 87; DB 2; Length 330;
 Best Local Similarity 20.4%; Pred. No. 0.95;

Matches 44; Conservative 29; Mismatches 53; Indels 90; Gaps 11;

QY 33 FHNG---GVOILCKPYDVOQFMOLKGGQILDLTKGK-----71
 D 71 FHNGRSIRSOVASY---TFKATVNDSEYRCOMEQTRLSQVLDGVISDWLLQTPQ 125
 QY 72 ---GNVSIKSLKFCQSOLSN--NSVSFF-----LYNLDHSNANYE 108
 D 126 LVFLBETITLR---CHSWRNKLNRISEFHNKSVRYHHYSSNFSIPKRNHSHSGDY 181
 QY 109 CNLS---IFDPPPKVTLTGGLHYESOLCCQKFWLPI-----GCAAFVVCIL 156
 D 182 CKGSLGRTHOSKPVITVQGP-----KSSRSPLVLTIVAAYVGIIVAIL 230
 QY 157 GCILICMLTKKKYSSVHDPN-----GEY 180
 D 231 --VSLVYLKKQVPALPGNPDHREMGETLPEEYGEY 264

RESULT 14

hypothetical protein F52H2.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Jun-2000
 C/Accession: T32479
 R/Chisoe, S.; Hawkins, J.
 Submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid F52H2.
 A/Reference number: 221175
 A/Accession: T32479
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-563 <CHT>
 A/Cross-references: EMBL:AF026214; PIDN:AA71312.1; GSPDB:GN00028; CESP:F52H2.2
 A/Experimental source: strain Bristol N2; clone F52H2
 C/Genetics:
 A/Map position: X
 A/Introns: 20/3; 60/1; 123/2; 162/1; 204/1; 255/2; 296/3; 329/1; 401/2; 433/3; 544/1
 C/Superfamily: arginine peptidase

Query Match 8.0%; Score 87; DB 2; Length 563;
 Best Local Similarity 24.1%; Pred. No. 1.7;

Matches 52; Conservative 24; Mismatches 58; Indels 82; Gaps 12;

QY 8 FELFLRKIKVLTGEINGSANYEMFFHNGVOI--LCKYPDIVGOQFMOLK-----G 58
 D 305 WFAFCMPFVACSTI--GSAN-----GVILRLTGSRDVROAIAEVAEPQNPRTFG 354
 QY 59 GOILCDLTKTKSGSNVSIKSLKFC-----SOLSNVSFFLYNLDHSNANYEFC 109
 D 355 NROLPNLTSOKIFGN---ROLPEFNEFVEIIFLSALEKSMVVFPPS-----ETLFGC 405
 QY 110 -----NLSTFDPPPKVTLTG---GYL-----HIYESOLCCQKFWLPIGC 147
 D 406 GAREGQMPNVLTVNKTTPRIP-AVILTGLSLYLILSNINYSILNYIGVSWIAIG 464
 QY 148 A-----AFVVCIGCILI 161
 D 465 AIALFPRKTMPPAPRAVKAPIVPIIFIFGCVLL 500

RESULT 15

A29063
 cytotoxic T-lymphocyte protein 4 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
 C/Accession: A29063; I49622
 R/Brunner, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.
 Nature 328, 267-270, 1987
 A>Title: A new member of the immunoglobulin superfamily--CTLA-4.
 A/Reference number: A29063; MUID:87258255
 A/Accession: A29063

A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-223 <BRU>
 A/Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593
 R/Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Goldstein, P.
 J. Immunol. 147, 1037-1044, 1991
 A>Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
 A/Reference number: I49584; MUID:91318145
 A/Accession: I49622
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-36 <RES>
 A/Cross-references: GB:M74362; NID:g192833; PIDN:AAA37489.1; PID:g553903
 C/Genetics:
 A/Map position: 1, band C
 C/Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C/Keywords: transmembrane protein

Query Match 8.0%; Score 86.5; DB 2; Length 223;
 Best Local Similarity 19.5%; Pred. No. 0.69; Mismatches 7;
 Matches 36; Conservative 34; Indels 23; Gaps 7;

```

OY 1 M K S G L W Y F - - F L P C L R I K V L T G E I N S A N Y E M F I H N G V Q I L C K Y P - - - - - D I V 48
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 L P S R T W P F V A L L T L F I P F S E A I Q V T Q P S V L A S S H G V A S F P C E Y S P S H N T D E V R V T L 74
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 49 Q O F K M Q L I K G G O I I C D I T K T K S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F 108
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 75 K Q T M D Q M T E - - - - V C A T T F T E - - K N T V G F L D Y P C S G T F N E S R V N L T I O G L R A V D T G L Y L 128
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 109 C N L S I F D P P P P K V T L - T G G Y L H I Y E S O L C C Q L K F - - W L - - P I G C A F V V V C I L G C I L I C W 163
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 129 C K V E L M T P P P Y E G M G N G T Q I Y I D P E P C P D S D F L M I I V A V S L G L F Y S F L V S A V S L S K 188
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 164 L T K R K 168
    | | | | |
Db 189 M L K R R 193
    | | | | |
  
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Search completed: October 21, 2002, 07:47:20
 Job time : 24 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 : Search time 12 Seconds
(without alignments)
642.099 Million cell updates/sec

Title: US-09-823-307C-2

Perfect score: 1082

Sequence: 1 MKSGMYTFLECLRIKVLTG.....YMFRAVNTAKSRDLTVIL 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No	Score	Query Match	Length	DB ID	Description
1	159	14.7	218	1	CD28_RAT
2	150.5	13.9	221	1	CD28_RABIT
3	141.1	13.0	219	1	CD28_MOUSE
4	139.5	12.9	220	1	CD28_HUMAN
5	138	12.8	218	1	CD28_MOUSE
6	97	9.0	221	1	CD28_CHICK
7	89	8.2	321	1	OSV1_HUMAN
8	86.5	8.0	330	1	FCG2_MOUSE
9	86	7.9	223	1	CTL4_MOUSE
10	82.5	7.6	248	1	VEG2_EBV
11	81	7.5	1382	1	ME1_RAT
12	81	7.5	1584	1	YJ9G_YEAST
13	77.5	7.2	324	1	CRFB_SHEEP
14	77.5	7.2	1070	1	PTK7_HUMAN
15	76.5	7.1	223	1	CTL4_RABIT
16	76.5	7.1	323	1	FCG2_HUMAN
17	76.5	7.1	317	1	FCG2_HUMAN
18	76	7.0	448	1	BCN1_MOUSE
19	76	7.0	450	1	BCN1_MOUSE
20	76	7.0	450	1	BCN1_MOUSE
21	76	7.0	450	1	BCN1_MOUSE
22	76	7.0	450	1	BCN1_MOUSE
23	75.5	6.9	462	1	CANC_MOUSE
24	75	6.9	462	1	CANC_MOUSE
25	75	6.9	462	1	CANC_MOUSE
26	74.5	6.9	462	1	CANC_MOUSE
27	74	6.8	344	1	AD24_MOUSE
28	74	6.8	344	1	AD24_MOUSE
29	74	6.8	344	1	AD24_MOUSE
30	73.5	6.8	344	1	AD24_MOUSE
31	73.5	6.8	344	1	AD24_MOUSE
32	73.5	6.8	344	1	AD24_MOUSE
33	73.5	6.8	344	1	AD24_MOUSE

34	73.5	6.8	497	1	GRB_HUMAN	P48167	homo sapien
35	73.5	6.8	1162	1	EXEN_CLOBU	O06366	clostridium
36	73	6.7	275	1	YD84_YEAST	O12359	saccharomyc
37	73	6.7	916	1	SCR8_LIMPO	O25386	limulus pol
38	72.5	6.7	654	1	BPR2_HUMAN	O01742	homo sapien
39	72	6.7	561	1	AIAD_RAT	P23944	rattus norv
40	72	6.7	569	1	YJ53_YEAST	O06567	saccharomyc
41	71.5	6.6	634	1	YKX3_EUGER	P31916	euglena gra
42	71.5	6.6	1051	1	PRK7_CHICK	O91048	gallus gall
43	71	6.6	212	1	KITH_ENCCU	O96720	cephalifo
44	71	6.6	466	1	AIAD_BOVIN	P18130	bos taurus
45	70.5	6.5	524	1	VIL1_HPV58	P26535	human papil

ALIGNMENTS

RESULT 1	ID	CD28_RAT	STANDARD:	PRT:	218 AA.
AC	P31042:				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DE	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	T-cell-specific surface glycoprotein CD28 precursor.				
GN	CD28.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=DA; TISSUE=Lymphoid;				
RC	MEDLINE=92104640; PubMed=1309509;				
RA	Clark G.J., Dallman M.J.;				
RT	*Identification of a cDNA encoding the rat CD28 homologue.;				
RL	Immunogenetics 35:54-57(1992).				
CC	- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1				
CC	AND B7-2 (B70).				
CC	- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.				
CC	- SUPRACELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.				
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; X55288; GAA39003.1; -				
DR	PIR; S38722; S38722.				
DR	InterPro; IPR003600; I9-like.				
DR	SMART; SM00410; IG-like; 1.				
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.				
FT	SIGNAL	1	19		
FT	CHAIN	20	218		
FT	CD28.				
FT	DOMAIN	20	150		
FT	DOMAIN	151	177		
FT	POTENTIAL.				
FT	EXTRACELLULAR (POTENTIAL).				
FT	CYTOPLASMIC (POTENTIAL).				
FT	IG-LIKE V-TYPE DOMAIN.				
FT	DOMAIN	178	218		
FT	DOMAIN	29	138		
FT	CARBOHYD	72	72		
FT	CARBOHYD	93	93		
FT	CARBOHYD	106	106		
FT	CARBOHYD	130	130		
FT	CARBOHYD	130	130		
FT	SEQUENCE	218 AA:	25170 MM;		
FT	SEQUENCE	218 AA:	25151C85324C0B6E CRC04;		

Query Match 14.78; Score 159; DB 1; Length 218;
Best Local Similarity 26.5%; Pred. No. 2.1e-08;
Matches 41; Conservative 30; Mismatches 66; Indels 18; Gaps 7;

OY 30 MEFFHNGVOILCKYPD--IVQOFKMOILKGOILCDLTKRGSGNTVSIKSLK-----F 82
 DB 29 LLVVNNNEVSLCKRYXNLDHSHANYFECNLSTFDPPEP--KVTLTGLYHIEESOLC-- 86
 OY 83 CHSOLSNNSVSFFLYXNDHSHANYFECNLSTFDPPEP--KVTLTGLYHIEESOLC--C 137
 DB 87 CDGFMDEMTYFRLMNDVHNDIYFKIEVMFPPLIDNEKSNGTIIRKKEHCHAOI 146
 OY 138 QLKFWLPIGCAFYVNC--ILGCLLIC--WLTKKK 168
 DB 147 SPLKFWPLVYVAGVLLCYGLLVTVLCTITWTSRR 181
 RESULT 2
 ID CD28_RABIT STANDARD; PRT; 221 AA.
 AC P42069;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T-cell-specific surface glycoprotein CD28 precursor.
 GN CD28.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed-7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 CC AND B7-2 (B70) (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: D49841; BAA08641.1;
 DR InterPro: IPR003600; I9_1like.
 DR SMART: SM00410; Ig-like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
 FT CHAIN 1 19
 FT SIGNAL 1 19
 FT DOMAIN 20 150
 FT TRANSMEM 151 177
 FT DOMAIN 178 221
 FT DOMAIN 221 138
 FT CARBOHYD 38 38
 FT CARBOHYD 72 72
 FT CARBOHYD 93 93
 FT CARBOHYD 106 106
 FT CARBOHYD 130 130
 SO SEQUENCE 221 AA; 25307 MW; 3DF652C9CFC14F13 CRC64;
 Query Match 13.9%; Score 150.5; DB 1; Length 221;
 Best Local Similarity 23.8%; Pred. No. 1.4e-07;
 Matches 38; Conservative 27; Mismatches 70; Indels 25; Gaps 6;
 OY 30 MEFFHNGVOILCKYPD--IVQOFKMOILKGOILCDLTKRTGS-----GNTVSIKSL 80

DB 29 LLVVNNNEVSLCKRYXNLDHSHANYFECNLSTFDPPEP--KVTLTGLYHIEESOLC-- 86
 OY 81 KCFHSOLSNNSVSFFLYXNDHSHANYFECNLSTFDPPEP--KVTLTGLYHIEESOLC-- 136
 DB 87 --CDGKRGNTYFRLMNDVHNDIYFKIEVMFPPLIDNEKSNGTIIRKKEHCHAOI 144
 OY 137 -----COLKFWPL--GCAAFYVNCILGCLLICWLTKKK 168
 DB 145 HPSFKSTLFWLVVAGVLLCYGLLVTVLCTITWTSRR 184
 RESULT 3
 ID CD28_BOVIN STANDARD; PRT; 219 AA.
 AC Q28071;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T-cell-specific surface glycoprotein CD28 precursor.
 GN CD28.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96186531; PubMed-8606060;
 RX Parsons K.R., Young J.R., Collins R.A., Howard C.J.;
 RT "Cattle CTLA-4, CD28 and chicken CD28 bind CD86: mypwy is not
 RT conserved in cattle CD28.";
 RL Immunogenetics 43:388-391(1996).
 CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 CC AND B7-2 (B70).
 CC -1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X93304; CAA63707.1;
 DR InterPro: IPR003600; I9_1like.
 DR SMART: SM00410; Ig-like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.
 FT CHAIN 1 18
 FT SIGNAL 1 18
 FT DOMAIN 19 151
 FT TRANSMEM 152 178
 FT DOMAIN 179 219
 FT DOMAIN 219 136
 FT CARBOHYD 37 37
 FT CARBOHYD 71 71
 FT CARBOHYD 84 84
 FT CARBOHYD 91 91
 FT CARBOHYD 104 104
 FT CARBOHYD 128 128
 SO SEQUENCE 219 AA; 25143 MW; 85B5C50E96634AA CRC64;
 Query Match 13.0%; Score 141; DB 1; Length 219;
 Best Local Similarity 23.2%; Pred. No. 1.2e-06;
 Matches 36; Conservative 32; Mismatches 71; Indels 16; Gaps 6;
 OY 30 MEFFHNGVOILCKYPD--IVQOFKMOILKGOILCDLTKRTGS--GNTVSIKSLKF-CHS 85

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OM protein - protein search, using sw model

Run on: October 21, 2002, 07:46:28 ; Search time 31 seconds
(without alignments)
713.022 Million cell updates/sec

Title: US-09-823-307C-2

Sequence: 1 MKSGWYFFFLCKRLKVLTLG.....YMFRAVNTAKRNLDTVL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0 747574

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1082	100.0	199	19 AAW75956	Human cell surface
2	1082	100.0	199	19 AAW75957	Human cell surface
3	1082	100.0	199	20 AAW80826	Human activated T-
4	1082	100.0	199	21 AAB08731	Amino acid sequenc
5	1082	100.0	199	22 AAE03428	Human gene 2 encod
6	1082	100.0	199	22 AAE03460	Human gene 2 encod
7	1082	100.0	199	22 AAE03525	Human secreted pro
8	1066.5	98.6	198	21 AAY92213	Human Th2-specific
9	737.5	68.2	200	21 AAY92212	Murine Th2-specific
10	734	67.8	200	21 AAB08723	Amino acid sequenc
11	722.5	66.8	200	19 AAW75958	Human cell surface

12	701	64.8	200	19 AAW71874	Rat cell surface p
13	696	64.3	216	19 AAW71875	Rat cell surface p
14	658	60.8	379	22 AAB67716	Amino acid sequenc
15	449.5	41.5	380	22 AAB67717	Amino acid sequenc
16	146.5	13.5	225	20 AAY41136	Rat CD28 protein s
17	145.5	13.4	221	21 AAY32286	Feline CD28. Feli
18	145.5	13.4	221	21 AAY32279	cat CD28 receptor.
19	139.5	12.9	220	13 AAR20805	Human CD28 antigen
20	139.5	12.9	220	13 AAR27103	Sequence encoded b
21	139.5	12.9	220	17 AAR02131	Human CD28 CDNA pr
22	139.5	12.9	220	17 AAR91433	Human CD28 antigen
23	139.5	12.9	220	16 AAW84413	CD28. Homo sapien
24	139.5	12.9	220	19 AAW80442	Human CD28 antigen
25	139.5	12.9	220	20 AAW84451	Human CD28 antigen
26	139.5	12.9	220	21 AAY96128	Human CD28 recepto
27	139.5	12.9	220	21 AAY44294	Human CD28 recepto
28	139.5	12.9	220	22 AAU02437	Human CD28 protein
29	134	12.4	225	20 AAY41135	Mouse CD28 protein
30	126	11.6	225	20 AAY41137	Human CD28 protein
31	120.5	11.1	367	18 AAW35862	Human CD28.19G2a c
32	119.5	11.0	152	16 AAW35846	Human CD28.19G2a c
33	119.5	11.0	134	18 AAW35846	Human CD28.19G2a c
34	89.5	8.3	305	22 AAY24469	Human CD28 extracell
35	89	8.2	319	22 AAG71916	Human partial oifa
36	89	8.2	321	22 AAG71916	Human olfactory re
37	89	8.2	319	22 AAG71916	Human OLFXY protei
38	87.5	8.1	213	22 AAE04561	Human G-protein co
39	87	8.0	330	8 AAY70445	Sequence of mouse
40	86	7.9	223	18 AAW25111	Soluble human CTLA
41	86	7.9	223	22 AAG66519	Human CTLA4. Homo
42	86	7.9	223	22 AAU00687	Human CTLA4. protei
43	85.5	7.9	187	19 AAW29728	Soluble CTLA4 muta
44	84.5	7.8	209	21 AAY94998	Human secreted pro
45	84	7.8	223	21 AAY15129	Human CTLA-4 prote

ALIGNMENTS

RESULT 1	AAW75956	standard. Protein: 199 AA.
ID	AAW75956	
XX	AC	
XX	AAW75956:	
XX	11-DEC-1998 (first entry)	
XX	Human cell surface protein #1.	
XX	Human: cell surface protein: thymocyte; lymphocyte: cell adhesion;	
KW	signal transmission; autoimmune disorder; allergy; diagnosis;	
KW	mitogen-stimulated.	
XX		
XX	Homo sapiens.	
XX	OS	
XX	PN	WO9838216-A1.
XX	PD	
XX	03-SEP-1998.	
XX	PF	27-FEB-1998: 98MO-JP00837.
XX	PR	26-FEB-1998: 98JP-0062217.
XX	PR	27-FEB-1997: 97JP-0062290.
XX	PA	(NISH) JAPAN TOBACCO INC.
XX	PI	Tamatori T, Tezuka K;
XX	PI	
XX	DR	WPI: 1998-481144/41.
XX	DR	N-PSDB: AAW53198.
XX	XX	
PT	Cell surface molecule expressed in thymocytes and lymphocytes and -	
PT	mediating signal transmission and cell adhesion, and antibodies to	

PT It useful in treatment of auto:immune and allergic disorders.
 XX
 PS Claim 2; Page 99-101; 149pp; Japanese.
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDDPPF in its extracellular region and the
 CC sequence YMM in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SO Sequence 199 AA:
 Query Match 100.0%; Score 1082; DB 19; Length 199;
 Best Local Similarity 100.0%; Pred.No. 6.6e-116; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 0;
 QY 1 M K S G L W F F L F C L R I K V L G E I N G S A N Y E M F I F H N G V O I L C K Y P D I V O Q F K M O L L K G Q 60
 Db 1 M K S G L W F F L F C L R I K V L G E I N G S A N Y E M F I F H N G V O I L C K Y P D I V O Q F K M O L L K G Q 60
 QY 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P K 120
 Db 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P K 120
 QY 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T R K K Y S S V H D P N G E Y 180
 Db 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T R K K Y S S V H D P N G E Y 180
 QY 181 M F M R A V N T A K K S R L T D V T L 199
 Db 181 M F M R A V N T A K K S R L T D V T L 199
 RESULT 2
 ID AAM75957 standard; Protein: 199 AA.
 XX AAM75957;
 AC
 DT 11-DEC-1998 (first entry)
 DE Human cell surface protein #2.
 KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 OS Homo sapiens.
 XX
 OS WO9838216-A1.
 PN
 XX
 PD 03-SEP-1998.
 PF
 XX 27-FEB-1998; 98WO-JP00837.
 XX
 PR 26-FEB-1998; 98JP-0062217.
 PR 27-FEB-1997; 97JP-0062290.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 PI Tamatani T, Tezuka K;
 XX WPI: 1998-481144/41.
 DR N-PSDB: AAV53199.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto:immune and allergic disorders.

XX
 PS Claim 9; Page 101-105; 149pp; Japanese.
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDDPPF in its extracellular region and the
 CC sequence YMM in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SO Sequence 199 AA:
 Query Match 100.0%; Score 1082; DB 19; Length 199;
 Best Local Similarity 100.0%; Pred.No. 6.6e-116; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 0;
 QY 1 M K S G L W F F L F C L R I K V L G E I N G S A N Y E M F I F H N G V O I L C K Y P D I V O Q F K M O L L K G Q 60
 Db 1 M K S G L W F F L F C L R I K V L G E I N G S A N Y E M F I F H N G V O I L C K Y P D I V O Q F K M O L L K G Q 60
 QY 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P K 120
 Db 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P P K 120
 QY 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T R K K Y S S V H D P N G E Y 180
 Db 121 V T L T G Y L H I E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T R K K Y S S V H D P N G E Y 180
 QY 181 M F M R A V N T A K K S R L T D V T L 199
 Db 181 M F M R A V N T A K K S R L T D V T L 199
 RESULT 3
 ID AAY08026 standard; Protein: 199 AA.
 XX AAY08026;
 AC
 DT 08-JUL-1999 (first entry)
 DE Human activated T-lymphocyte protein 8F4.
 KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
 KW T cell activation; cytokine synthesis; regulatory element; B cell;
 KW T cell-dependent antibody production; treatment; prevention; cancer;
 KW autoimmune disease; transplant rejection; immune system regulation;
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
 OS Homo sapiens.
 XX
 OS WO9915553-A2.
 PN
 XX
 PD 01-APR-1999.
 PF
 XX 23-SEP-1998; 98WO-DE02896.
 XX
 PR 11-MAY-1998; 98DE-1021060.
 PR 23-SEP-1997; 97DE-1041929.
 XX
 PA (DEKO-) DEUT KOCH INST ROBERT.
 XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
 PI Kroczeck R;
 XX
 XX WPI: 1999-276975/23.
 DR N-PSDB: AAX37661.
 XX

PF polypeptide 8p4 co-stimulates T cells and is present only on
 activated cells
 Claim 2, Page 24, 47pp; German.
 CC This invention describes a novel human protein, 8p4, and its encoding
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
 CC monocytes, natural killer or dendritic cells. 8p4 has anticancer,
 CC antiviral, anti-asthma and immunomodulatory activity. 8p4 provides a
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
 CC proliferation of T cells, synthesis of certain cytokines and other
 CC regulatory agents, and improves T cell-dependent antibody production
 CC by B cells. Agents that inhibit 8p4 are used to treat or prevent
 CC autoimmune diseases, to prevent transplant rejection and to treat
 CC disorders of immune system regulation. 8p4 of cells that express it,
 CC is/are used to treat or prevent cancers, acquired immune deficiency
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
 CC
 SO Sequence 199 AA:
 Y Match 100.0%; Score 1082; DB 20; Length 199;
 Best Local Similarity 100.0%; Pred. No. 6.6e-116;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M K S G L W F F L F C R I K V L T G E I N G S A N Y E M F I P H N G V O I L C K Y P D I V O O F K M O L L K G Q 60
 DB 1 I L C D L R T K G S G M T V S I K S L K F C H S O L S N N S V S F F L Y N D H S H A N Y F C N L S I F D P P P R K 120
 DB 61 I L C D L R T K G S G M T V S I K S L K F C H S O L S N N S V S F F L Y N D H S H A N Y F C N L S I F D P P P R K 120
 QY 121 V T L T G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K R K S S V H P N G E Y 180
 DB 121 V T L T G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K R K S S V H P N G E Y 180
 QY 181 M F M R A V N T A K K S R L T D V T L 199
 DB 181 M F M R A V N T A K K S R L T D V T L 199
 Db 181 M F M R A V N T A K K S R L T D V T L 199
 RESULT 4
 ID AAB08731
 AAB08731 standard; Protein; 199 AA.
 AC AAB08731;
 XX
 Dm 02-JAN-2001 (first entry)
 X Amino acid sequence of a human CRP1 polypeptide.
 DL
 XX CRP1: CD28 related protein-1; B7RP1, B7 related protein-1;
 KM T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KM T cell proliferation; T-cell mediated disorder.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 FT Domain 21..199
 FT /note= "extracellular domain"
 FT Domain 141..161
 FT /note= "predicted transmembrane domain"
 FT Domain 162..199
 FT /note= "intracellular domain"
 PN WO2000046240-A2.
 XX 10-AUG-2000.

XX 27-JAN-2000; 2000WO-US01871.
 PF 03-FEB-1999; 99US-0244448.
 PR 08-MAR-1999; 99US-0264527.
 XX (AMGE-) AMGEN INC.
 PA yoshinaga SK;
 PI WPI: 2000-543476/49.
 DR N-PSDB; AAA64558.
 XX
 PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 XX Disclosure; Fig 13A; 174pp; English.
 PS
 CC The present sequence represents a CRP1 (CD28 related protein-1)
 CC polypeptide. The specification also describes a B7RP1 (B7 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 CC
 SO Sequence 199 AA:
 Query Match 100.0%; Score 1082; DB 21; Length 199;
 Best Local Similarity 100.0%; Pred. No. 6.6e-116;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 M K S G L W F F L F C R I K V L T G E I N G S A N Y E M F I P H N G V O I L C K Y P D I V O O F K M O L L K G Q 60
 DB 1 M K S G L W F F L F C R I K V L T G E I N G S A N Y E M F I P H N G V O I L C K Y P D I V O O F K M O L L K G Q 60
 DB 61 I L C D L R T K G S G M T V S I K S L K F C H S O L S N N S V S F F L Y N D H S H A N Y F C N L S I F D P P P R K 120
 DB 61 I L C D L R T K G S G M T V S I K S L K F C H S O L S N N S V S F F L Y N D H S H A N Y F C N L S I F D P P P R K 120
 QY 121 V T L T G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K R K S S V H P N G E Y 180
 DB 121 V T L T G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K R K S S V H P N G E Y 180
 QY 181 M F M R A V N T A K K S R L T D V T L 199
 DB 181 M F M R A V N T A K K S R L T D V T L 199
 Db 181 M F M R A V N T A K K S R L T D V T L 199
 RESULT 5
 ID AAE03428
 AAE03428 standard; Protein; 199 AA.
 AC AAE03428;
 XX
 Dm 10-AUG-2001 (first entry)
 X Human gene 2 encoded secreted protein HT2SG64, SEQ ID NO: 111.
 DL
 XX Human: secreted protein; proliferative disorder; cancer; tumour; asthma;
 KM foetal abnormality; developmental abnormality; haematopoietic disorder;
 KM immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KM Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
 KM psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
 KM inflammation; neurological disorder; Alzheimer's disease; food additive;
 KM angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;
 KM pregnancy-related disorder; endocrine disorder; infection; wound healing;
 KM cell culture; chemotaxis; vulnerability; binding partner identification;
 KM gene therapy.
 XX

OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers
FT	1..19
FT	/label=Signal_peptide
FT	Protein
FT	20..111
XX	/note="Mature human secreted protein"
FN	MO200132675-A1.
XX	
PD	10-MAY-2001.
XX	
PF	25-OCT-2000; 2000MO-US29363.
PR	
PR	29-OCT-1999; 99US-0162239.
PR	30-JUN-2000; 2000OUS-0215139.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
XX	Ruben SM, Komatsualls GA, Wei P, Baker KP, Young PE;
Lr	WPI: 2001-328772/34.
DR	N-PSDB: AAD07810.
XX	
PT	Thirty two human secreted proteins, useful for treating cancers,
PT	hyperproliferative disorders, inflammatory disorders, neurological
PT	disorders, autoimmune diseases and cardiovascular disorders -
XX	
PS	Claim 11; Page 471; 576pp; English.
CC	AAD07809-AA007907 represent cDNAs corresponding to 32 human secreted
CC	protein genes, and AA003427-AA03323 represent the proteins they encode.
CC	AA003324-AA03337 represent human secreted protein fragments or variants.
CC	The secreted proteins and their genes are useful for preventing, treating
CC	or ameliorating medical conditions, e.g., by protein or gene therapy of the
CC	new protein in sample or by determining the presence of mutations in
CC	the new genes. Specific uses are described for each of the 32 genes,
CC	based on the tissues in which they are most highly expressed, and include
CC	developing products for the diagnosis or treatment of proliferative
CC	diseases, cancer, tumours, foetal and developmental abnormalities,
CC	hematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC	neurological disorders (e.g., rheumatoid arthritis), inflammation, allergies,
CC	cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC	psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC	angio-genetic disorders, kidney disorders, gastrointestinal disorders,
CC	pregnancy-related disorders, endocrine disorders, and infections. The
CC	proteins can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues, to identify their cognate ligands or binding
CC	partners, and in chemotaxis, and can be used as a food additive or
CC	preservative to modify storage properties. Antibodies specific for a
CC	protein of the invention can be used in alleviating symptoms associated
CC	with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC	radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC	The present sequence represents a human secreted protein of
CC	the invention.
XX	
XX	Sequence 199 AA:
QY	Query Match 100.0%, Score 1082; DB 22; Length 199;
QY	Best Local Similarity 100.0%, Pred. NO. 6.e-116;
Dh	Matches 199; Conservative 0%; Mismatches 0; Indels 0; Gaps 0;
QY	1 MKSGLWFFFLFCRIKIVLTGELINGSANYEMFIFNAGGVQILCKYPDVIQDFKMQLKGQ 60
Db	1 MKSGLWFFFLFCRIKIVLTGELINGSANYEMFIFNAGGVQILCKYPDVIQDFKMQLKGQ 60
QY	1 ILCDLITFKSGGWTVSIRKSILKFSCHOLSNNNSVSPFLYLMLDISHSHANYFCNLSTIDPPPK 120
Db	1 ILCDLITFKSGGWTVSIRKSILKFSCHOLSNNNSVSPFLYLMLDISHSHANYFCNLSTIDPPPK 120

OY		121	VTTGGVLIHTYESQGLCOLKFMFLPICAFVWVCILGCLITLMTKKRSSVHPDNEY	180
DB		121	VTLLGTGLIHTYESQLCOLKFMFLPICAFVWVCILGCLITLMTKKRSSVHPDNEY	180
OY		181	MENRANVTAKKSRLPYDTL	199
DB		181	MENRANVTAKKSRLPYDTL	199
RESULT 6				
AAE03460				
ID	AAE03460	standard; Protein; 199 AA.		
XX				
AC	AAE03460;			
DT	10-AUG-2001	(first entry)		
XX				
DE	Human gene 2 encoded secreted protein HRZSG64, SEQ ID NO: 143.			
XX				
KW	Human; secreted protein; proliferative disorder; cancer; tumour; asthma;			
KW	focal abnormality; developmental abnormality; haematopoietic disorder;			
KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;			
KW	Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;			
KW	psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;			
KW	inflammation; neurological disorder; Alzheimer's disease; food additive;			
KW	angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;			
KW	pregnancy-related disorder; endocrine disorder; infection; wound healing;			
KW	cell culture; chemotaxis; vulnery; binding partner identification;			
gene therapy.				
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Peptide	1..19		
FT	/label= Signal_peptide	20..199		
FT	Protein	/note= "Mature human secreted protein"		
PN		WC0200132675-A1.		
XX				
PD		10-MAY-2001.		
XX				
PF		25-OCT-2000; 200OWO-US92563.		
XX				
PR		29-OCT-1999; 99US-0162239.		
PR		30-JUN-2000; 200OUS-0215139.		
PA	(HGMA-) HUMAN GENOME SCI INC.			
PI	Ruben SM, Komatsu S G A, Wei P, Baker KP, Young PE;			
DR	WPI: 2001-338772/34.			
XX	N-PSDS: AAD07842.			
PT	Thirty two human secreted proteins, useful for treating cancers,			
PT	hyperproliferative disorders, inflammatory disorders, neurological			
PT	disorders, autoimmune diseases and cardiovascular disorders -			
XX				
XX	Claim 11; Page 489-490; 576pp; English.			
XX				
XX	AAD07809-AA007907, represent cDNAs corresponding to 32 human secreted			
CC	protein genes, and AAE03427-AAED03523 represent the proteins they encode.			
CC	AAED03524-AAED03537 represent human secreted protein fragments or variants.			
CC	The secreted proteins and their genes are useful for preventing, treating,			
CC	or ameliorating medical conditions, e.g., by protein or gene therapy.			
CC	Pathological conditions can be diagnosed by determining the amount of the			
CC	new protein in a sample or by determining the presence of mutations in			
CC	the new genes. Specific uses are described for each of the 32 genes,			
CC	based on the tissues in which they are most highly expressed, and include			
CC	developing products for the diagnosis or treatment of proliferative			
CC	hematopoietic disorders, diseases of the immune system, AIDS, autoimmune			
CC	hematopoietic disorders, tumours, foetal and developmental abnormalities,			
CC	hematopoietic disorders, diseases of the immune system, AIDS, autoimmune			

Homo sapiens.
OS
XX
FH FH Key .location/Qualifiers
FT FT Peptide /label= conserved_PPP_motif 113..118
FT FT /note= "common in CD28 and CTLA-4"
FT FT Peptide 178..181
FT FT /label=YXMM_motif
FT FT /note= "common in CD28 and CTLA-4; necessary for
CD28-mediated phosphatidylinositol 3-kinase activity"

WO200019986-A1.

XZ XZ 13-APR-2000.

XX XX PF 06-OCT-1999; 99WO-US23156.

XX XX PR 07-OCT-1998; 98US-0168229.

XX XX PR 26-FEB-1999; 99US-0258670.

XX XX PR 06-OCT-1999; 99US-0413136.

(MILL-) MILLENNIUM PHARM INC.

PJ Lehar S., Manning S., Coyle AJ, Gutierrez-Ramos J;
PI WPT; 2000-303619/26.
DR N-PDB; AAA09056.

XX PT T helper (Th) 2 nucleic acids and encoded proteins, useful for the
PT diagnosis and treatment of immune and respiratory disorders such as
PT Crohn's diseases, arthritis, insulin dependent diabetes and
autoimmunity

Claim 16; Page 138-139; 159pp; English.

CC CC This Th2-specific polypeptide, which has similarity to human CD28 and
CC human CTRP-4, is encoded by human orthologue h1228.
CC A novel method for modulating a Th2 response, an immune response, or
CC suppressing airway inflammation or hyperresponsiveness in a mammal,
CC comprises administering a Th2 specific polipeptide of the invention, an
CC antibody to such a polipeptide or allelic variants of the genes. The
CC novel DNA and polipeptide sequences are useful for treatment and
CC diagnosis of Th cell and Th cell-like disorders such as Crohn's disease,
CC atthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
CC bacterial infections (including human immunodeficiency virus (HIV)),
CC viral infections, bronchitis, cystic fibrosis, diphtheria,
CC emphysema, pneumonia, and Legionnaires disease.

SQ Sequence 198 AA:

Query Match 98.6%; Score 1066.5; DB 21; Length 198;

Best Local Similarity 99.5%; Pred.No.3.9e-114;

Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1

OY 1 MSKGLWFFFLFCRIKRVLTGGEINGSANTEMFIFHNHGVOIIICXPDIYOOKMKLKGGO 60
Db ||||||
OY 1 MKSGMWFEFLFCRIKVLTGGEINGSANTEMFIFHNNGVGIICKIPDITVOGRFKMLKKGG 60
Db ||||||

OY 61 ILDDLRKTGSQGNTVSIRKLKFCHQSLSNNSVPFLYLMDHSNANYFCNLSTFDPEPRK 120
Db ||||||

OY 61 ILCDDRKTGSQNMTVISIKLKLFCHQSLSNNSVFPLYLDHSHANYTFCNLSTFDPPPFR 120
Db |||||

OY 121 VTLTGATLAHTESQLCCLRWPLIGCAAFVVYVCILGCILCIWLTKKKRYSSVDHPNGEY 180
Db |

Db	121	VTLLGGYLIHAIRESOLCCOLKFMFLPGCAAFVVCILICILICMLT-KKYSVVHPDNGEY 179
Qy	181	MEMRAVNTAKKSRLLDYTL 199
Db	180	MEMRAVNTAKKSRLLDYTL 198
RESULT 9		
AA992212		
AA92212		
AA92212		standard; Protein; 200 AA.
AA92212:		
10-AUG-2000		(first entry)
Murine Th2-specific polypeptide, m128.		
m128; Th2-specific; T helper cell; anti-inflammatory; antiarthritic; CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological; antiproliferative; antiallergic; anti-viral; ophthalmological; CTLA-4; nephrotropic; anti-HIV; antibacterial.		
Mus musculus.		
Key		Location/Qualifiers
Peptide	114..119	/label= conserved_ppp_motif
		/note= "common in CD28 and CTLA-4"
Peptide	181..184	/label= YXXM_motif
		/note= "common in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity"
MO200019988-A1.		
13-APR-2000.		
06-OCT-1999;	99MO-US23156.	
07-OCT-1998;	98US-0168329.	
26-FEB-1999;	99US-0258670.	
06-OCT-1999;	99US-0413136.	
(MILL-) MILLENNIUM PHARM INC.		
Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;		
WPI: 2000-303619/26.		
N-PSDB: AAA09054.		
T helper (Th) 2 nucleic acids and encoded proteins, useful for the diagnosis and treatment of immune and respiratory disorders such as Crohn's diseases, arthritis, insulin dependent diabetes and autoimmunity		
Claim 16; Page 130-131; 159pp; English.		
This Th2-specific polypeptide is encoded by a murine orthologue m1288.		
The protein shares homology with both human and murine CD28 and CTLA-4.		
A novel method for modulating a Th2 response, an immune response, or suppressing airway inflammation or hyperresponsiveness in a mammal comprises administering a Th2-specific polypeptide of the invention, an antibody to such a polypeptide or allelic variants of the genes. The novel DNA and polypeptide sequences are useful for treatment and diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases, arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis, dermatitis, psoriasis, graft rejection, graft versus host diseases, sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis, viral infections (including human immunodeficiency virus (HIV)), bacterial infections, bronchitis, cystic fibrosis, diptheria, emphysema, pneumonia, and Legionnaires disease.		

XX Sequence 200 AA; Score 737.5; DB 21; Length 200;
 Query Match Best Local Similarity 69.3%; Pred. No. 2.4e-76;
 Matches 138; Conservative 20; Mismatches 40; Indels 1; Gaps 1;

QY 1 M K S G L M Y F F L C L R I K V L G E I N S A N Y E M F I F H N G S V O I L C K Y P D I V O O F K M Q L K G G Q 60
 1 M K P Y C H V F E C F L R L T L G E I N S A D H R M F S F H N G S V O I S C K Y P E T V O O L K M R L F R E R 60
 DB 1 M K P Y C H V F E C F L R L T L G E I N S A D H R M F S F H N G S V O I S C K Y P E T V O O L K M R L F R E R 60

OY 61 I L C D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P F K V 120
 61 V L C E L T K T K G S G N A V S I K N P M L C L Y H L S N N S V S F L N N P D S S G S Y F C S L S I F D P P F Q 120

OY 121 V - T T G G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K K Y S S V H D P N G E 179
 121 E R N I S G G Y L H I Y E S O L C C O L K M L P V G C A F V V V L F G C I L I I M F S K K Y G S S V H D P N S E 180

DB 121 E R N I S G G Y L H I Y E S O L C C O L K M L P V G C A F V V V L F G C I L I I M F S K K Y G S S V H D P N S E 180

OY 180 Y M P M R A V N T A K S R L T D V T 198
 181 Y M P M A V N T N K S R L A G V T 199

RESULT 10
 AAB08723 standard; Protein; 200 AA.
 AAB08723;
 02-JAN-2001 (first entry)

DE Amino acid sequence of a murine CRP1 polypeptide.
 KW CRP1, CD28 related protein-1; B7RP1; B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KW T cell proliferation; T-cell mediated disorder.
 XX Mus sp.

OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..20 /note="signal peptide"
 FT Protein 21..200 /note="mature protein"
 FT Domain 21..145 /note="extracellular domain"
 FT Domain 146..163 /note="predicted transmembrane domain"
 FT Domain 164..200 /note="intracellular domain"

W0200046240-A2.
 10-AUG-2000.
 27-JAN-2000: 2000OWO-US01871.
 03-FEB-1999: 99US-0244448.
 08-MAR-1999: 99US-0264527.
 (AMGE-) AMGEN INC.
 Yoshinaga SK;
 WPI: 2000-543476/49.
 N-PSDB: AAA64554.
 Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 in the treatment, prevention and diagnosis of T cell mediated disorders
 Claim 11; Fig 1A; 174pp; English.

XX The present sequence represents a CRP1 (CD28 related protein-1)
 CC polypeptide. The specification also describes a B7RP1 (B7 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.

SO Sequence 200 AA; Score 734; DB 21; Length 200;
 Query Match Best Local Similarity 70.4%; Pred. No. 5.9e-76;
 Matches 138; Conservative 19; Mismatches 35; Indels 4; Gaps 2;

OY 7 Y F - - F L C L R I K V L G E I N S A N Y E M F I F H N G S V O I L C K Y P D I V O O F K M Q L K G G Q I L C 63
 4 Y F C R V F E C F L R L T L G E I N S A D H R M F S F H N G S V O I S C K Y P E T V O O L K M R L F R E R E V L C 63

DB 64 D L T K T K G S G N T V S I K S L K F C H S O L S N N S V S F F L Y N L D H S H A N Y F C N L S I F D P P F K V - T 122
 64 E L T K T K G S G N A V S I K N P M L C L Y H L S N N S V S F L N N P D S S G S Y F C S L S I F D P P F Q E R N 123

OY 123 L T G G Y L H I Y E S O L C C O L K F M L P I G C A F V V V C I L G C I L I C M L T F K K Y S S V H D P N G E Y M F 182
 124 L S G G Y L H I Y E S O L C C O L K M L P V G C A F V V V L F G C I L I I M F S K K Y G S S V H D P N S E Y M F 183

DB 183 M R A V N T A K S R L T D V T 198
 184 M A A V N T N K S R L A G V T 199

RESULT 11
 AAW75958 standard; Protein; 200 AA.
 AAW75958;
 11-DEC-1998 (first entry)

DE Mouse cell surface protein.
 KW Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transduction; autoimmune disorder; allergy; diagnosis;
 KW mltigen-stimulated.
 XX Mus sp.

OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..20 /note="signal peptide"
 FT Protein 21..200 /note="mature protein"
 FT Domain 21..145 /note="extracellular domain"
 FT Domain 146..163 /note="predicted transmembrane domain"
 FT Domain 164..200 /note="intracellular domain"

W09838216-A1.
 03-SEP-1998.
 27-FEB-1998: 98WO-JP00837.
 26-FEB-1998: 98JP-0062217.
 27-FEB-1997: 97JP-0062290.
 (NISB) JAPAN TOBACCO INC.
 Tamatani T, Tezuka K;
 WPI: 1998-481144/41.
 N-PSDB: AAV53200.
 Cell surface molecule expressed in thymocytes and lymphocytes and -
 mediating signal transduction and cell adhesion, and antibodies to
 it useful in treatment of autoimmune and allergic disorders.
 Claim 9; Page 110-112; 149pp; Japanese.
 The present sequence represents a mouse cell surface protein which is

CC antibodies recognising the cell surface protein. These antibodies also
CC produce an increase in peripheral blood lymphocytes in the presence of
CC an antibody recognising CD3 antigen. The cell surface protein contains
CC the amino acid sequence FDPPPF in its extracellular region and the
CC sequence YFWM in its intracellular region. The cell surface protein can
CC be used in the prevention and treatment of autoimmune and allergic
CC diseases, and in the diagnosis and investigation of such disorders.
XX
SQ Sequence 216 AA:
Query Match 64.3%; Score 696; DB 19; Length 216;
Best Local Similarity 68.8%; Pred. No. 1.5e-71;
Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;
OY 7 YF---FLFCLRIKIVLGEINGSANYEMFIFHNGVOILCKYPIVOQFPMOLKGGQILIC 63
DB 4 YFSCVFEVFCFLIKLITGLNDLANHMFSPHOGVOISCNYPETVQOLKMLFKDREVLIC 63
OY 64 DLKRTGSGNTVSIKSLKCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFDPPPF-KYT 122
DB 64 DLKRTGSGNTVSIKSLKCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFDPPPFQEKX 123
OY 123 LINGXYLHYESOLCCOLKMLPIGCAAFVYVCLIGLILCWLTKKYSSVDPNGEYMF 182
DB 124 LSGGILLITLIESQLCCQKMLPVGCAAFVAAALFGCLITWFRKKYSSVDPNSEYMF 183
OY 183 MRAVNTAKKSRL 194
DB 184 MAAVNTNKKSRLL 195
RESULT 14
AAB67716
ID AAB67716 standard; Protein; 379 AA.
AC AAB67716;
XX
DT 11-JUN-2001 (first entry)
XX
DE Amino acid sequence of hICOS-mig2am fusion protein.
XX
KW GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus musculus.
XX
P J0200121796-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000MO-US25892.
XX
PR 21-SEP-1999; 99US-0155043.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Ling V, Dunnasi-Joannopolulos K;
XX
DR WPI: 2001-244938/25.
XX
DR N-PSDB: AAF79939.
XX
PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a
XX
PS Immune response and reducing the proliferation of a tumour cell -
XX
PS Disclosure; Fig 26B; 195pp; English.
XX
CC The present sequence represents a fusion protein, comprising human ICOS
CC (hICOS) and murine IgG2a (mig2a). The fusion protein is used in the
CC course of the invention. The specification describes GL50 polypeptides.
CC GL50 molecules are antigens on the surface of antigen presenting cells,

CC which costimulate T cell proliferation and bind to costimulatory receptor
CC ligands on T cells. GL50 modulating agents are used to modulate an immune
CC response in a subject. GL50 polypeptides are used to modulate T cell
CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC that can be treated using GL50 molecules are graft-versus-host disease,
CC autoimmune disease, allergies, acquired immune deficiency syndrome
CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC GL50 polynucleotides can be used to locate gene regions associated with
CC genetic disease, in tissue typing, and in forensic identification of a
CC biological sample.
XX
SQ Sequence 379 AA:
Query Match 60.8%; Score 658; DB 22; Length 379;
Best Local Similarity 100.0%; Pred. No. 7.4e-67;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 21 FINSNANYEMFIFHNGVOILCKYPIVOQFPMOLKGGQILCDLTKGSGNTVSIKSL 80
DB 26 FINSNANYEMFIFHNGVOILCKYPIVOQFPMOLKGGQILCDLTKGSGNTVSIKSL 85
OY 81 KFCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFDPPPFVTLTGGLHYESOLCCOLK 140
DB 86 KFCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFDPPPFVTLTGGLHYESOLCCOLK 145
OY 141 F 141
DB 146 F 146
RESULT 15
AAB67717
ID AAB67717 standard; Protein; 380 AA.
AC AAB67717;
XX
DT 11-JUN-2001 (first entry)
XX
DE Amino acid sequence of mICOS-mig2am fusion protein.
XX
KW GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine.
XX
OS Synthetic.
OS Mus musculus.
XX
P W0200121796-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000MO-US25892.
XX
PR 21-SEP-1999; 99US-0155043.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Ling V, Dunnasi-Joannopolulos K;
XX
DR WPI: 2001-244938/25.
XX
DR N-PSDB: AAF79940.
XX
PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a
XX
PS Immune response and reducing the proliferation of a tumour cell -
XX
PS Disclosure; Fig 27B; 195pp; English.
XX
CC The present sequence represents a fusion protein, comprising murine ICOS
CC (mICOS) and murine IgG2a (mig2a). The fusion protein is used in the
CC course of the invention. The specification describes GL50 polypeptides.
CC GL50 molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory receptor
CC ligands on T cells. GL50 modulating agents are used to modulate an immune

CC response in a subject. GL50 polypeptides are used to modulate T cell
 CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
 CC that can be treated using GL50 molecules are graft-versus-host disease,
 CC autoimmune disease, allergies, acquired immune deficiency syndrome
 CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
 CC GL50 polynucleotides can be used to locate gene regions associated with
 CC genetic disease, in tissue typing, and in forensic identification of a
 CC biological sample.
 XX

SO Sequence 380 AA:

Query Match 41.5%; Score 449.5; DB 22; Length 380;
 Best Local Similarity 70.2%; Pred No. 6,5e-43;
 Matches 85; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 21 EINGSNAYEMPIFNGGVOLCKYDPDIYQOFKMLKGOIICDLTKTKSGNTVSIKSL 80
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 26 EINGSAHHRFSPHNGVQLCKYDPDIYQOFKMLKGOIICDLTKTKSGNTVSIKSL 85
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 81 KFCISQISNNNSVSFFLYNLDSHANYFCNLSTFDPPPKV-TLTGGLHIYESQLCOL 139
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 86 MLCIYHLSNNSVSFFLYNLDSHANYFCNLSTFDPPPKV-TLTGGLHIYESQLCOL 145
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 140 K 140
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Search completed: October 21, 2002, 07:48:51
 Job time : 34 secs